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OM protein - protein search, using sw model

Run on: August 14, 2003, 18:06:36 ; Search time 47 Seconds

2134.366 Million cell updates/sec

Title: US-10-040-906A-2

Sequence: 1 MNNVLNNGRTTICDAYNVA.....GTQFELMNIMFVPTNLPPIY 632

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1. A_gensedc135tund3.*
2. /SIDS1/gcgatc/geneseq/geneeqp-emb1/AA1980.DAT.*
3. /SIDS1/gcgatc/geneeq/geneeqp-emb1/AA1981.DAT.*
4. /SIDS1/gcgatc/geneeq/geneeqp-emb1/AA1982.DAT.*
5. /SIDS1/gcgatc/geneeq/geneeqp-emb1/AA1983.DAT.*
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12. /SIDS1/gcgatc/geneeq/geneeqp-emb1/AA1990.DAT.*
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14. /SIDS1/gcgatc/geneeq/geneeqp-emb1/AA1992.DAT.*
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19. /SIDS1/gcgatc/geneeq/geneeqp-emb1/AA1997.DAT.*
20. /SIDS1/gcgatc/geneeq/geneeqp-emb1/AA1998.DAT.*
21. /SIDS1/gcgatc/geneeq/geneeqp-emb1/AA1999.DAT.*
22. /SIDS1/gcgatc/geneeq/geneeqp-emb1/AA2000.DAT.*
23. /SIDS1/gcgatc/geneeq/geneeqp-emb1/AA2001.DAT.*
24. /SIDS1/gcgatc/geneeq/geneeqp-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	331.4	100.0	632	22	AAU02021	B. thuringiensis t
2	3048.5	92.0	633	15	AA856696	Cyrlia insecticida
3	3046.5	91.9	635	22	AAU02043	B. thuringiensis t
4	3043.5	91.8	634	21	AA94559	Cy2Aa delta-endot
5	3015.5	91.0	635	19	AAW75772	Amino acid sequen
6	3010.5	90.8	633	21	AA948460	Cy2Ab delta-endot
7	3005.5	90.7	634	21	AA948454	Cy2Ab delta-endot
8	2974.5	89.8	633	13	AA920030	Bacillus thuringie
9	2914.5	87.9	633	19	AAW75775	Amino acid sequen

45	307	9.3	1157	20	AAW84586
44	307	9.3	1157	15	AAW84582
43	307	9.3	1157	10	AAW84582
42	307	9.3	1157	5	AAW84582
41	308	9.3	1157	20	AAW84592
40	308	9.3	1157	20	AAW84588
39	308	9.3	1157	20	AAW84588
38	308	9.3	1157	20	AAW84583
37	309	9.3	1157	20	AAW84581
36	309	9.3	1157	20	AAW84580
35	309	9.3	1157	20	AAW84584
34	310	9.4	1157	20	AAW84580
33	310.5	9.4	719	22	AAW84583
32	311	9.4	1157	20	AAW84587
31	311.5	9.4	1156	22	AAU02034
30	311.5	9.4	1156	20	AAW24960
29	311.5	9.4	1156	19	AAW46857
28	311.5	9.4	1156	19	AAW46857
27	314.5	9.8	719	22	AAU02095
26	324.5	9.8	719	21	ABO7073
25	324.5	9.8	719	11	AAW08041
24	324.5	9.8	719	11	AAW08041
23	325	9.8	719	11	AAW08041
22	325.5	9.8	719	22	AAW66997
21	325.5	9.8	719	22	AAW66997
20	327.5	9.9	719	22	AAW66998
19	327.5	9.9	719	22	AAW66998
18	331.5	10.0	710	22	AAU02041
17	336.5	10.2	643	10	AAW81356
16	336.5	10.2	643	10	AAW81356
15	1089	15.1	99	9	AAW81356
14	1089	15.1	99	9	AAW81356
13	1274.5	38.5	250	9	AAW83002
12	1274.5	38.5	250	9	AAW83002
11	2610.5	78.8	623	19	AAW5774
10	2610.5	78.8	623	19	AAW5774
9	2913.5	87.9	633	19	AAW5773
8	2913.5	87.9	633	19	AAW5773
7	2952.5	77.9	625	22	AAU02004
6	2952.5	77.9	625	22	AAU02004
5	14	32.6	706	18	AAW11189
4	14	32.6	706	18	AAW11189
3	14	32.6	706	18	AAW11189
2	14	32.6	706	18	AAW11189
1	14	32.6	706	18	AAW11189

ALIGNMENTS

	RESULT 1
ID	AAU02021
PI	AAU02021 standard; Protein; 632 AA.
AC	AAU02021;
NC	
XX	29-AUG-2001 (first entry)
D7T	
XX	
DE	B. thuringiensis toxic crystal protein, CryET11.
XX	
KM	Delta endotoxin; lepidopteran-active; crystal protein; insecticide;
KM	transgenic plant; corn; wheat; soybean; oat; cotton; rice; sorghum
KM	sugarcane; tomato; tobacco; kapok; flax; potato; barley; turf grass;
KM	pasture grass; berry; fruit; legume; vegetable; ornamental plant; shrub
KM	cactus; tree cell; gypsy moth; looper; tobacco budworm; spruce budworm;
XX	cotton leaf perforator; CryET11.
XX	
OS	Bacillus thuringiensis.
XX	
PN	WO200119859-A2.
PD	
XX	22-MAR-2001.
XX	
XX	13-SEP-2000; 2000WO-US25361.
PP	
PR	15-SEP-1999; 99US-0153995.
XX	
PA	(MONS) MONSANTO CO.
XX	
PI	
XX	
BAUM JA,	Chiu C, Donovan WP, Gilmer AJ, Rupar MJ;
WIPI,	2001-281518/29.
OR	

DR N-PSDB; AAS02464.
 XX Lepidopteran-active Bacillus thuringiensis delta-endotoxin polypeptides
 PT and the polynucleotides that encode them, useful for increasing the
 PT insect resistance of plant -
 XX
 XX Claim 5; Page 102-103; 173pp; English.
 XX
 CC The sequence represents a B. thuringiensis Lepidopteran-active
 CC delta-endotoxin, crystal protein CryET31. The Lepidopteran-active B.
 CC thuringiensis delta-endotoxin polypeptides may be used as compositions
 CC that are applied to plant crops to protect them from insect damage. The
 CC polynucleotides may be used in the production of transgenic plants that
 CC express the insecticidal polypeptides and consequently have improved
 CC insect resistance compared to non-transformed plants. Monocotyledonous or
 CC dicotyledonous plants may be protected in this way, for example corn,
 CC wheat, soybean, oat, cotton, rice, rye, sorghum, sugarcane, tomato,
 CC tobacco, kapok, flax, potato, barley, turf grass, pasture grass, berry,
 CC fruit, legume, vegetable, ornamental plant, shrub, cactus and/or tree
 CC cell. A wide range of insects (e.g. gypsy moth, looper, tobacco budworm,
 CC cotton leaf perforator and spruce budworm) may be affected by application
 CC of the insecticidal polypeptides (full details given in specification).
 XX
 XX Sequence 632 AA:
 SQ
 Query Match 100.0%; Score 3314; DB 22; Length 632;
 - Best Local Similarity 100.0%; Pred. No. 3,76-259;
 Matches 632; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2
 AAR5696
 ID AAR5696 standard; Protein; 633 AA.
 XX
 XX AAR5696;
 AC
 DT 25-MAR-2003 (updated)
 DT 27-MAR-1995 (first entry)
 XX
 DE CryIIA insecticidal crystal protein.
 XX
 KW CryIIA; CryIIIA; CryIIB; CryC; P-2; CryBI; insecticidal protein crystal;
 KW lepidoptera; environmental insecticide; Bacillus thuringiensis; toxic;
 KW probe; hybridisation.
 XX
 OS Bacillus thuringiensis.
 XX
 PN US539544-A.
 PD 16-AUG-1994.
 XX
 XX 26-FEB-1993; 93US-0023736.
 XX
 XX 16-APR-1987; 87US-0039542.
 PR 11-JUL-1989; 89US-0379015.
 PR 28-AUG-1991; 91US-0751452.
 PR 26-FEB-1993; 93US-0023736.
 XX
 PA (ECOG-) ECOGEN INC.
 XX
 PI Donovan WP;
 XX
 XX WPI; 1994-263236/32.
 DR N-PSDB; AAO71025.
 DR
 XX New Cry IIB protein - obtd. from the cry II B gene in Bacillus
 PT thuringiensis var. Kurstaki, active against lepidopteran insects
 XX
 PS Example 2; Fig 2A-2C; 39pp; English.
 XX
 CC This sequence shows the amino acid sequence of CryIIA protein.
 CC The CryIIA gene was used as a probe to identify CryIIA related
 CC sequences, ie. CryIIB. CryIIB encodes an insecticidal crystal
 CC protein isolated from Bacillus thuringiensis var. Kurstaki. It
 CC produces crystal proteins during sporulation which are specifically
 CC toxic to certain orders and species of insects, esp. lepidopterans.
 CC CryIIB can be used in compositions used as environmentally acceptable
 CC insecticides. (See also AAR5697-8) PF field.)
 CC
 CC (Updated on 25-MAR-2003 to correct PF field.)
 CC
 SQ Sequence 633 AA;
 Query Match 92.0%; Score 3048.5; DB 15; Length 633;
 - Best Local Similarity 90.7%; Pred. No. 1,1e-237;
 Matches 574; Conservative 34; Mismatches 24; Indels 1; Gaps 1;

QY 241 MLEPRTYMLNFEVYVSIWLSFKYQSLVSSGANTYASGSGPOQTOSTSQDMPFLYSLP 300
 DB 241 MLEPRTYMLNFEVYVSIWLSFKYQSLVSSGANTYASGSGPOQTOSTSQDMPFLYSLP 300
 QY 301 QVNSNYLVNGFSGARLTQTFPNIGGLPGTTTHALLARVYVSGVSGDIGAV-FNQN 359
 DB 301 QVNSNYLVNGFSGARLTQTFPNIGGLPGTTTHALLARVYVSGVSGDIGAV-FNQN 359
 QY 360 SCSTFPLPLTFPVYVWLDSDRGVNTVWQTESFESTLGLRCGAFYARNSNPPD 419
 DB 361 NCSTVLPPLSTFPVYVWLDSDRGVNTVWQTESFESTLGLRCGAFYARNSNPPD 420
 QY 420 YFRNLSGVLVVRNEDLRPLHNEIRNIESPSTPGGRLAYVWSVHNRKNNIYAHEH 479
 DB 421 YFRNLSGVLVVRNEDLRPLHNEIRNIESPSTPGGRLAYVWSVHNRKNNIYAHEH 480
 QY 480 GTWHLAPEDYTGFTISPIHATOVNNQRTFISEKFGQDSLRFGQSTTARVTLRGNG 539
 DB 481 GTWHLAPEDYTGFTISPIHATOVNNQRTFISEKFGQDSLRFGQSTTARVTLRGNG 540
 QY 540 NSVNLVLRVSSLGSTIRVTINGRVYVTAENVTTTNDGVNDGARFDDIMNGVVASDN 599
 DB 541 NSVNLVLRVSSLGSTIRVTINGRVYVTAENVTTTNDGVNDGARFDDIMNGVVASDN 600
 QY 600 TNPVLDINTFNSGTQFELNIMFVPTNLPPIY 632
 DB 601 TNPVLDINTFNSGTQFELNIMFVPTNLPPIY 633

RESULT 3
 AAU02043
 ID AAU02043 standard; Protein, 635 AA.
 AC AAU02043;
 DT 29-AUG-2001 (first entry)
 XX
 XX B. thuringiensis toxic crystal protein, CryET72.
 XX
 XX Delta endotoxin; Lepidopteran-active; crystal protein; insecticide;
 KW transgenic plant; corn; wheat; soybean; oat; cotton; rice; rye; sorghum;
 KW sugarcane; tomato; tobacco; kapok; flax; potato; barley; turf grass;
 KW pasture grass; berry; fruit; legume; vegetable; ornamental plant; shrub;
 KW cactus; tree cell; gypsy moth; looper; tobacco budworm; spruce budworm;
 KW cotton leaf perforator; CryET72.
 XX
 XX Bacillus thuringiensis.
 OS
 XX
 XX WO200119859-A2.
 PN
 XX
 XX 22-MAR-2001.
 PD
 XX
 XX 13-SEP-2000; 2000WO-US25361.
 PF
 XX
 XX 15-SEP-1999; 99US-0153995.
 PR
 XX
 XX (MONS) MONSANTO CO.
 PA
 XX
 XX Baum JA, Chu C, Donovan WP, Gilmer AJ, Rupar MJ;
 PI
 XX
 XX WPI; 2001-281518/29.
 DR
 XX
 XX N-PSDB; AAS02486.
 XX
 XX
 XX Claim 5; Page 158-160; 173pp; English.
 PS
 XX
 XX The sequence represents a B. thuringiensis lepidopteran-active
 CC delta-endotoxin, crystal protein CryET72. The lepidopteran-active B.
 CC thuringiensis delta-endotoxin polypeptides may be used as compositions
 CC that are applied to plant crops to protect them from insect damage. The

CC polynucleotides may be used in the production of transgenic plants that
 CC express the insecticidal polypeptides and consequently have improved
 CC insect resistance compared to non-transformed plants. Monocotyledonous or
 CC dicotyledonous plants may be protected in this way, for example corn,
 CC wheat, soybean, oat, cotton, rice, rye, sorghum, sugarcane, tomato,
 CC tobacco, kapok, flax, potato, barley, turf grass, pasture grass, berry,
 CC fruit, legume, vegetable, ornamental plant, shrub, cactus and/or tree
 CC cell. A wide range of insects (e.g. gypsy moth, looper, tobacco budworm,
 CC cotton leaf perforator and spruce budworm) may be affected by application
 CC of the insecticidal polypeptides (full details given in specification).

Sequence 635 AA;

Query Match 91.98; Score 3046.5; DB 22; Length 635;

Best Local Similarity 90.98; Pred. No. 1.ee-237;

Matches 577; Conservative 31; Mismatches 24; Indels 3; Gaps 2;

QY 1 MNNVLANGRRTTICDANYVVAHDPFSEHKSIDTRKEMEMKRTDHSIYVAVTVGSF 60
 DB 1 MNNVLANGRRTTICDANYVVAHDPFSEHKSIDTRKEMEMKRTDHSIYVAVTVGSF 60
 QY 61 LKKTGSLIGKRLISELMGLIPSGSTNLMQDLRBTQFLNQLNDTTLARVNAELBL 120
 DB 61 LKKTGSLIGKRLISELMGLIPSGSTNLMQDLRBTQFLNQLNDTTLARVNAELBL 120
 QY 61 LKKTGSLIGKRLISELMGLIPSGSTNLMQDLRBTQFLNQLNDTTLARVNAELBL 120
 DB 61 LKKTGSLIGKRLISELMGLIPSGSTNLMQDLRBTQFLNQLNDTTLARVNAELBL 120
 QY 121 QANIREFNOQVDNFPNPNVPLSITSSVNTMOQFLRLPOFVVOGYLLPLPFAA 180
 DB 121 QANIREFNOQVDNFPNPNVPLSITSSVNTMOQFLRLPOFVVOGYLLPLPFAA 180
 QY 181 ANHLSFTRDYVLANDBNGISAATRTYQNTLKNYTRYTSNCINTYQYARGLNTRLMD 240
 DB 181 ANHLSFTRDYVLANDBNGISAATRTYQNTLKNYTRYTSNCINTYQYARGLNTRLMD 240
 QY 241 MLEPRTYMLNFEVYVSIWLSFKYQSLVSSGANTYASGSGPOQTOSTSQDMPFLYSLP 300
 DB 241 MLEPRTYMLNFEVYVSIWLSFKYQSLVSSGANTYASGSGPOQTOSTSQDMPFLYSLP 300
 QY 301 QVNSNYLVNGFSGARLTQTFPNIGGLPGTTTHALLARVYVSGVSGDIGAV-FNQN 359
 DB 301 QVNSNYLVNGFSGARLTQTFPNIGGLPGTTTHALLARVYVSGVSGDIGAV-FNQN 359
 QY 360 SCSTFPLPLTFPVYVWLDSDRGVNTVWQTESFESTLGLRCGAFYARNSNPPD 419
 DB 361 NCSTVLPPLSTFPVYVWLDSDRGVNTVWQTESFESTLGLRCGAFYARNSNPPD 420
 QY 418 PDYFRNLSGVLVVRNEDLRPLHNEIRNIESPSTPGGRLAYVWSVHNRKNNIYAHEH 479
 DB 421 PDYFRNLSGVLVVRNEDLRPLHNEIRNIESPSTPGGRLAYVWSVHNRKNNIYAHEH 480
 QY 478 ENGTMHILAPEDYTGFTISPIHATOVNNQRTFISEKFGQDSLRFGQSTTARVTLRGNG 539
 DB 481 ENGTMHILAPEDYTGFTISPIHATOVNNQRTFISEKFGQDSLRFGQSTTARVTLRGNG 540
 QY 538 NGSNYLVLRVSSLGSTIRVTINGRVYVTAENVTTTNDGVNDGARFDDIMNGVVASDN 599
 DB 541 NGSNYLVLRVSSLGSTIRVTINGRVYVTAENVTTTNDGVNDGARFDDIMNGVVASDN 600
 QY 598 DNTNVPVLDINTFNSGTQFELNIMFVPTNLPPIY 632
 DB 601 DNTNVPVLDINTFNSGTQFELNIMFVPTNLPPIY 633

RESULT 4
 AA94259
 ID AA94259 standard; Protein, 634 AA.
 AC AA94259;
 DT 28-JUL-2000 (first entry)
 XX
 XX Cry2Aa delta-endotoxin.
 DE
 XX
 XX Transgenic plant; insect resistance; cry2Aa delta-endotoxin; Coleopteran;

Db 601 SDVPLDINVTLNNGTQFDLNMIMVPTNISPLY 633

RESULT 7
AAV94254 standard; Protein; 634 AA.

AAV94254;

28-JUL-2000 (first entry)

Cry2Ab delta-endotoxin.

Transgenic plant; insect resistance; cry2Ab delta-endotoxin; Coleopteran; Lepidopteran; Diptera; plasmid transit peptide; PTP; insecticidal; plasmid targeting peptide.

Bacillus thuringiensis.

WO200026371-A1.

11-MAY-2000.

04-NOV-1999; 99WO-US26086.

04-NOV-1998; 98US-0186002.

(MONS) MONSANTO CO.

Corbin DR, Romano CP;

WPI; 2000-376130/32.

N-PSDB; AAL5556.

New method of expressing insecticidal proteins in plants transformed with a *Bacillus thuringiensis* delta-endotoxin encoding gene resulting in effective control of susceptible target pests

Claim 14; Page 82-83; 104pp; English.

The present sequence is the Cry2Ab delta-endotoxin. Delta-endotoxins are produced by *Bacillus thuringiensis* during sporulation. These proteins are toxic to certain species of insect e.g. Lepidopteran and Coleopteran larvae. An insect-resistant transgenic plant has been constructed which contains the cry2Ab gene. The cry2Ab gene would be transferred into plants via expression vectors, which subsequently allow high expression of the cry2Ab gene. The present sequence lacks Dipteran inhibitory activity. Protection may be attained against insects such as *Oscitina* spp., *Diatraea* spp., *Helicoverpa* spp., and *Spodoptera* spp., in *Zea mays*; *Heliothis virescens*, *Helicoverpa* spp., *Pectinophora* spp., in *Gossypium hirsutum*; *Anticarsa* spp., *Pseudoplusia* spp., *Epilachna* spp., in *Glycine max*; and *Scirpophaga incertulas* in *Oryza sativa*. Expression of the cry2Ab gene by a plant cell produces a fusion protein comprising an amino-terminal plasmid transit peptide (PTP) covalently linked to the delta-endotoxin. The fusion protein functions to localise the delta-endotoxin to a subcellular organelle or compartment.

Sequence 634 AA;

Query Match 90.7%; Score 3005.5; DB 21; Length 634;
Best Local Similarity 89.7%; Pred. No. 3.3e-234;
Matches 567; Conservative 39; Mismatches 25; Indels 1; Gaps 1;

2 NNVLNNGRTTCDAYNVVAADPFSEHSLDTIRKEMWKRTHSLVYAPVGVSSFL 61
3 NSVLNNGRTTCDAYNVVAADPFSEHSLDTIRKEMWKRTHSLVYAPVGVSSFL 62
62 LKKVSLIGKRIISSEIMGLIFPSGSTNMODIIRTECPINORLNTTLARVAELRGO 121
63 LKKVSLIGKRIISSEIMGLIFPSGSTNMODIIRTECPINORLNTTLARVAELRGO 122
122 ANIRENQVNFNLPNTQNPVPLSTTSVNTMOQLNRLPQFVQGYQLLLPLFAQA 181

Db 123 ANVEENRQVDFNFANPNRNAPVLESTISSVNTMOQLNRLPQFVQGYQLLLPLFAQA 182
Qy 182 NMHLSPTRDVTNADENGISAATLRTYQNYLAKNTTETSYNCINTYQTRAFGLTRHLM 241
Db 183 NLHLSPTRDVTNADENGISAATLRTYQNYLAKNTTETSYNCINTYQTRAFGLTRHLM 242
Qy 242 LEFRTYMFNLVEEYVSIWSLFFKQSLVSSGANLYASGSGPQQTQSFTSQDMPYSLRQ 301
Db 243 LEFRTYMFNLVEEYVSIWSLFFKQSLVSSGANLYASGSGPQQTQSFTSQDMPYSLRQ 302
Qy 302 VNSVYVNLNGFSGARLSTFPFIVGLPGSTTHALLARVYSGGSSGDIQASFPNEN 362
Db 303 VNSVYVNLNGFSGARLSTFPFIVGLPGSTTHALLARVYSGGSSGDIQASFPNEN 362
Qy 361 CSTFPLPPLTPFVRSWLDSDGDRGVNTVYVNTWQTESFSTLGRGAPFARNGSNYPDY 420
Db 363 CSTFPLPPLTPFVRSWLDSDGDRGVNTVYVNTWQTESFSTLGRGAPFARNGSNYPDY 422
Qy 421 FTRISGVLVVRNEDLRPLATNEIRNIESPSTPGCLRAYVSVHNRKNYAVHENG 480
Db 423 FTRISGVLVVRNEDLRPLATNEIRNIESPSTPGCLRAYVSVHNRKNYAVHENG 482
Qy 481 TMHLAPEDYTGFTISPIHATVQNNQTRTFISEKFGQGSILFEQSNVTARVTLRNGN 540
Db 483 SMHLAPNDYTGFTISPIHATVQNNQTRTFISEKFGQGSILFEQSNVTARVTLRNGN 542
Qy 541 SYNLVLRVSSIGNSTIRVTNGRVYVYASVNTTNNQVNDNGARPLDINNANVVASDNT 600
Db 543 SYNLVLRVSSIGNSTIRVTNGRVYVYASVNTTNNQVNDNGARPLDINNANVVASDNT 602
Qy 601 NVPLDINVTLNNGTQFDLNMIMVPTNISPLY 632
Db 603 NVPLDINVTLNNGTQFDLNMIMVPTNISPLY 634

RESULT 8
AAR20030
ID AAR20030 standard; Protein; 633 AA.

AAR20030;

07-APR-1992 (first entry)

Bacillus thuringiensis CryIIB crystal toxin.

B.t. crystal protein; insecticide; Lepidoptera; larva; corn earworm;

Heliothis zea.

Bacillus thuringiensis.

US5073632-A.

17-DEC-1991.

11-JUL-1989; 89US-0379015.

11-JUL-1989; 89US-0379015.

16-APR-1987; 87US-0039542.

(ECOG-) ECOGEN INC.

Donovan WP;

WPI; 1992-016224/02.

N-PSDB; AAO20202.

Bacillus thuringiensis cryIb protein gene - used to obtain the protein for use as an insecticidal cpd. against lepidopteran insects
Disclosure; Fig 6; 30pp; English.

CC The cryIIb gene was isolated from a B.t. strain using the cryIIa
CC gene as probe. The cryIIb gene encodes a 633 amino acid protein of
CC calculated mol. wt. 70,749. The insecticidal toxin CryIIb is twice
CC as toxic as the CryIIa protein against the lepidopteran *Heliothis*
CC zea.

XX Sequence 633 AA;

Query Match 89.8%; Score 2974.5; DB 13; Length 633;
Best Local Similarity 88.8%; Pred. No. 1,1e-231;
Matches 562; Conservative 39; Mismatches 31; Indels 1; Gaps 1;

QY 1 MNNVYVNGRTTICDANNVVAHDPSPFHKSLDTIRKEMWKKRTDHSLYVPIVGVSSF 60
DB 1 MNSVNSGRTTICDANNVVAHDPSPFHKSLDTIRKEMWKKRTDHSLYVPIVGVSSF 60
QY 61 LKKVGSLLIGKRIISELMGLIFPSGSTNLMODILRETEPFLNORLNTDTLLARVAELEG 120
DB 61 LKKVGSLLIGKRIISELMGLIFPSGSTNLMODILRETEPFLNORLNTDTLLARVAELEG 120
QY 121 QANIRFNOQVDNFIPLNTPONPVLSTSSVNTMOQLFARLPQFRVGYQLLLPLFAQA 180
DB 121 QANVEEPRQVDNFIPLNTPONPVLSTSSVNTMOQLFARLPQFRVGYQLLLPLFAQA 180
QY 181 ANMHLSPTRDVYVLADEMGISAATLRTYQNTAKYTTESYNCINTYQTAFAFGINTRLHD 240
DB 181 ANMHLSPTRDVYVLADEMGISAATLRTYQNTAKYTTESYNCINTYQTAFAFGINTRLHD 240
QY 241 MLEFRTWFLNVEFYVINSLEFKYQSLVSSGANLYASGSGPOQTOSTSODMPLYSLF 300
DB 241 MLEFRTWFLNVEFYVINSLEFKYQSLVSSGANLYASGSGPOQTOSTSODMPLYSLF 300
QY 301 QVNSVYVNGFSGARLTQTFPNIGLPGTTTHALLAARVNSGVSAGDIGA-VFNQNF 359
DB 301 QVNSVYVNAFSGARLTQTFPNIGLPGTTTHALLAARVNSGVSAGDIGA-VFNQNF 360
QY 360 SCSFTLPLLTTPFRSWLDSGDRGVNTVNTMOTSFESTGLRCGAFARNSNYFPD 419
DB 361 NCSTLPLLTTPFRSWLDSGDRGVNTVNTMOTSFESTGLRCGAFARNSNYFPD 420
QY 420 YFIRNISGVPLVVRNEDLRPLHYNEIRNIESPSGTPGGLRAYVNSVNRKNIYVAHEN 479
DB 421 YFIRNISGVPLVVRNEDLRPLHYNEIRNIESPSGTPGGLRAYVNSVNRKNIYVAHEN 480
QY 480 GTMHLAPEDYTGFTTSPHATOVNNQRTTISKEFGNCGDSLREDSNTTARYTLRGNG 539
DB 481 GTMHLAPEDYTGFTTSPHATOVNNQRTTISKEFGNCGDSLREDSNTTARYTLRGNG 540
QY 540 NSYNYLYRVSISGNTIRVTINGRYVTAASNVTNTTNDGVNDNGARFIDINMGVVASDN 599
DB 541 NSYNYLYRVSISGNTIRVTINGRYVTAASNVTNTTNDGVNDNGARFIDINMGVVASDN 600
QY 600 TNPPLDYNVENSGTQELMNIIMFPTNLPPIY 632
DB 601 SDVPLDYNVTINSGTQELMNIIMVPTNISPLY 633

RESULT 9
AAW5775
ID AAW5775 standard; Protein; 633 AA.

XX AAW5775;
XX
XX
XX 02-DEC-1998 (first entry)

DE Amino acid sequence of lepidopteran-active 8612 toxin.

XX 8612 toxin; PCR; primer; amplification; *Bacillus thuringiensis*; probe;
KW lepidoptera; pest; pesticide; *Ostrinia nubilalis*; *Heliothis virescens*;
XX *Helicoverpa zea*; hybridisation.

XX *Bacillus thuringiensis*.
XX

PN M08940430-A1.
XX
XX 17-SEP-1998.
PD
XX
XX
XX 13-MAR-1998; 98WO-US05081.
PF
XX
XX 13-MAR-1997; 97US-0040512.
PR
XX
XX (MYCO) MYCOGEN CORP.
PA
XX
XX Muller-Cohn J, Narva KE, Schnepf HE;
PI
XX
XX WPI; 1998-506734/43.
DR
XX
XX N-PSDB; AAV52612.
PT
XX
XX New insecticidal *Bacillus thuringiensis* toxins - useful for
PT controlling lepidopteran pests, especially *Ostrinia nubilalis*,
PT *Heliothis virescens* and *Helicoverpa zea*
XX
XX Claim 5; Pages 36-38; 50pp; English.
PS
XX
XX This is the amino acid sequence of a novel *Bacillus thuringiensis* toxin
CC used in the method of the invention, to control lepidopteran pests.
CC The new toxins are useful as pesticides, especially for the control of
CC *Ostrinia nubilalis*, *Heliothis virescens*, and *Helicoverpa zea*. The
CC polynucleotide coding sequences are useful for recombinant expression
CC of the toxins and the primers, together with probes derived from the
CC new sequences, are useful for the identification and characterisation
CC of novel genes that encode pesticidal toxins.
SQ
Sequence 633 AA;
Query Match 87.9%; Score 2914.5; DB 19; Length 633;
Best Local Similarity 87.0%; Pred. No. 7.6e-227;
Matches 551; Conservative 44; Mismatches 37; Indels 1; Gaps 1;

QY 1 MNNVYVNGRTTICDANNVVAHDPSPFHKSLDTIRKEMWKKRTDHSLYVPIVGVSSF 60
DB 1 MNNVYVNGRTTICDANNVVAHDPSPFHKSLDTIRKEMWKKRTDHSLYVPIVGVSSF 60
QY 61 LKKVGSLLIGKRIISELMGLIFPSGSTNLMODILRETEPFLNORLNTDTLLARVAELEG 120
DB 61 LKKVGSLLIGKRIISELMGLIFPSGSTNLMODILRETEPFLNORLNTDTLLARVAELEG 120
QY 121 QANIRFNOQVDNFIPLNTPONPVLSTSSVNTMOQLFARLPQFRVGYQLLLPLFAQA 180
DB 121 QANVEEPRQVDNFIPLNTPONPVLSTSSVNTMOQLFARLPQFRVGYQLLLPLFAQA 180
QY 181 ANMHLSPTRDVYVLADEMGISAATLRTYQNTAKYTTESYNCINTYQTAFAFGINTRLHD 240
DB 181 ANMHLSPTRDVYVLADEMGISAATLRTYQNTAKYTTESYNCINTYQTAFAFGINTRLHD 240
QY 241 MLEFRTWFLNVEFYVINSLEFKYQSLVSSGANLYASGSGPOQTOSTSODMPLYSLF 300
DB 241 MLEFRTWFLNVEFYVINSLEFKYQSLVSSGANLYASGSGPOQTOSTSODMPLYSLF 300
QY 301 QVNSVYVNGFSGARLTQTFPNIGLPGTTTHALLAARVNSGVSAGDIGA-VFNQNF 359
DB 301 QVNSVYVLSGFGSGLFTTTPFNIGLPGTTTHALLAARVNSGVSAGDIGA-VFNQNF 360
QY 360 SCSFTLPLLTTPFRSWLDSGDRGVNTVNTMOTSFESTGLRCGAFARNSNYFPD 419
DB 361 NCSTLPLLTTPFRSWLDSGDRGVNTVNTMOTSFESTGLRCGAFARNSNYFPD 420
QY 420 YFIRNISGVPLVVRNEDLRPLHYNEIRNIESPSGTPGGLRAYVNSVNRKNIYVAHEN 479
DB 421 YFIRNISGVPLVVRNEDLRPLHYNEIRNIESPSGTPGGLRAYVNSVNRKNIYVAHEN 480
QY 480 GTMHLAPEDYTGFTTSPHATOVNNQRTTISKEFGNCGDSLREDSNTTARYTLRGNG 539
DB 481 GTMHLAPEDYTGFTTSPHATOVNNQRTTISKEFGNCGDSLREDSNTTARYTLRGNG 540
QY 540 NSYNYLYRVSISGNTIRVTINGRYVTAASNVTNTTNDGVNDNGARFIDINMGVVASDN 599

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Db      541 NSYNLYRVSSIGNSTIRVTINGRYTASNVTTTNDGNDGNAFSDINIGVAVASN 600
Qy      600 TNVPLDINVTNSGTOPELMANIMFVPTNLPPIY 632
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      601 SDVPLDINVTNLSGTQFDLMNIMLVPTNISPPLY 633

RESULT 10
AAW75774
ID      AAW75774 standard; Protein. 633 AA.
AC      AAW75774;
XX      02-DEC-1998 (first entry)
DT      Amino acid sequence of lepidopteran-active HD525 toxin.
XX      KM HD525 toxin; PCR; primer; amplification; Bacillus thuringiensis; probe;
XX      KM lepidoptera; pest; pesticide; Ostrinia nubilalis; Heliothis virescens;
XX      KM Helicoverpa zea; hybridisation.
XX      OS Bacillus thuringiensis.
XX      PN MO9840490-A1.
XX      BD 17-SEP-1998.
XX      PF 13-MAR-1998; 98WO-US05081.
XX      PR 13-MAR-1997; 97US-0040512.
XX      ZX (MYCO) MYCOGEN CORP.
XX      PI Muller-Cohn J, Narva KE, Schnepf HE;
XX      DR WPI; 1998-506734/43.
XX      DR N-PSDB; AAV52611.
XX      PT New insecticidal Bacillus thuringiensis toxins - useful for
XX      PT controlling lepidopteran pests, especially Ostrinia nubilalis,
XX      PT Heliothis virescens and Helicoverpa zea
XX      PS Claim 14; Pages 32-34; 50pp; English.
XX      CC This is the amino acid sequence of a novel Bacillus thuringiensis toxin
XX      CC used in the method of the invention, to control lepidopteran pests.
XX      CC The new toxins are useful as pesticides, especially for the control of
XX      CC Ostrinia nubilalis, Heliothis virescens, and Helicoverpa zea. The
XX      CC polynucleotide coding sequences are useful for recombinant expression
XX      CC of the toxins and the primers, together with probes derived from the
XX      CC new sequences, are useful for the identification and characterisation
XX      CC of novel genes that encode pesticidal toxins.
XX      SQ Sequence 633 AA;

Query Match      87.9%; Score 2913.5; DB 19; Length 633;
Best Local Similarity 87.2%; Pred. No. 9,1e-227;
Matches 552; Conservative 42; Mismatches 38; Indels 1; Gaps 1;

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Db      181 ANHLSPFRDVLINAEWEGISAAATLRTYONHLNRYRDSVNCIDTYQTAFRGNTRLHD 240
Qy      241 MEERTWPELVNPEVYSIWSLFKYSQSLVSSGANTYASGSGPOOTQSFSTQDWPFLYSLF 300
Db      241 MLEFPTWPELVNPEVYSIWSLFKYSQSLVSSGANTYASGSGPOOTQSFSTQDWPFLYSLF 300
Qy      301 OVNSNVYVLNPEVSGARLTQTFPNIGGLPQTTTHALLAARVYSGVSGSDI -GAVFNQNF 359
Db      301 OVNSNVYVLNPEVSGARLTQTFPNIGGLPQTTTHALLAARVYSGVSGSDI -GAVFNQNF 360
Qy      360 SCSTELPPLPLPPYRAGMLDSDGSGVNTVNTQTESFEFSTGLRCGAPFARGNSVYFPD 419
Db      361 NCSTISPLPLSTFVRIMLDSGSDRGVYTTVMQTESFEFSTGLRCGAPFARGNSVYFG 420
Qy      420 YFIRNISGVPLVRNEDLRRLPHNRYNIESGTPFGGLARVYVSHKNNIYAVHEN 479
Db      421 YFIRNISGVSLVRNEDLRRLPHNRYNIESGTPFGGLARVYVSHKNNIYAVHEN 480
Qy      480 GFMHIAPEEDYTGFTISPIHATOVNQTFTFISEKFGNQSILRFEQSNNTTARYTLRNG 539
Db      481 GFMHIAPEEDYTGFTISPIHATOVNQTFTFISEKFGNQSILRFEQSNNTTARYTLRNG 540
Qy      540 NSYNLYRVSSIGNSTIRVTINGRYTASNVTTTNDGNDGNAFSDINIGVAVASN 599
Db      541 NSYNLYRVSSIGNSTIRVTINGRYTASNVTTTNDGNDGNAFSDINIGVAVASN 600
Qy      600 TNVPLDINVTNSGTOPELMANIMFVPTNLPPIY 632
Db      601 SDVPLDINVTNLSGTQFDLMNIMLVPTNISPPLY 633

RESULT 11
AAW75773
ID      AAW75773 standard; Protein; 623 AA.
AC      AAW75773;
XX      DT 02-DEC-1998 (first entry)
XX      DE Amino acid sequence of lepidopteran-active HD573 toxin.
XX      KM HD573 toxin; PCR; primer; amplification; Bacillus thuringiensis; probe;
XX      KM lepidoptera; pest; pesticide; Ostrinia nubilalis; Heliothis virescens;
XX      KM Helicoverpa zea; hybridisation.
XX      OS Bacillus thuringiensis.
XX      PN MO9840490-A1.
XX      PD 17-SEP-1998.
XX      PF 13-MAR-1998; 98WO-US05081.
XX      PR 13-MAR-1997; 97US-0040512.
XX      PX (MYCO) MYCOGEN CORP.
XX      PI Muller-Cohn J, Narva KE, Schnepf HE;
XX      DR WPI; 1998-506734/43.
XX      DR N-PSDB; AAV52610.
XX      PT New insecticidal Bacillus thuringiensis toxins - useful for
XX      PT controlling lepidopteran pests, especially Ostrinia nubilalis,
XX      PT Heliothis virescens and Helicoverpa zea
XX      PS Claim 14; Pages 28-30; 50pp; English.
XX      CC This is the amino acid sequence of a novel Bacillus thuringiensis toxin
XX      CC used in the method of the invention, to control lepidopteran pests.
XX      CC The new toxins are useful as pesticides, especially for the control of
XX      CC Ostrinia nubilalis, Heliothis virescens, and Helicoverpa zea. The

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CC polynucleotide coding sequences are useful for recombinant expression
CC of the toxins and the primers, together with probes derived from the
CC new sequences, are useful for the identification and characterisation
CC of novel genes that encode pesticidal toxins.
XX

Sequence 623 AA;

Query Match 78.8%; Score 2610.5; DB 19; Length 623;
Best Local Similarity 80.3%; Pred. No. 2.9e-202;
Matches 508; Conservative 46; Mismatches 68; Indels 11; Gaps 6;

QY 1 MNVANNGRRTTICADYNNVADHPSEFHSKSLDTIRKEMEMKRTDLSLYVPIVGTSSSF 60
DB 1 MNVANNGRRTTICADYNNVADHPSEFHSKSLDTIRKEMEMKRTDLSLYVPIVGTSSSF 60
QY 61 LKRVGSLVGRKILSELQNLIFPSSGIDLMQELIRATEQPIQRLNADTLGRVNAELAGL 120
DB 61 LKRVGSLVGRKILSELQNLIFPSSGIDLMQELIRATEQPIQRLNADTLGRVNAELAGL 120
QY 121 QANIRENQOVNDFLNPONVPLSTSSVTMMQOLFLNLPQFRVQVQQLLLPLPQA 180
DB 121 QANVAFENRQOVNDFLNPONVPLSTSSVTMMQOLFLNLPQFRVQVQQLLLPLPQA 180
QY 181 ANNHLSFRIDVILNADDEMGISAATLTQNTLYKNTTESNYCINTYQTAARGLNRLHD 240
DB 181 ANNHLSFRIDVILNADDEMGISAATLTQNTLYKNTTESNYCINTYQTAARGLNRLHD 240
QY 241 MLEFRTYELNVEFVYSIMSLFKYQSLVSSGANLYASGSGPQOTQSTQDMPFLYSLF 300
DB 241 MLEFRTYELNVEFVYSIMSLFKYQSLVSSGANLYASGSGPQOTQSTQDMPFLYSLF 300
QY 301 QVNSVYVNLGSGARLTQTPNIGLPGTTTHALLAARVNSGVSIGDGA-AYNNQNF 359
DB 299 QVNSVYVNLGSGARLTQTPNIGLPGTTTHALLAARVNSGVSIGDGA-AYNNQNF 358
QY 360 SCSTFLPPLLPFVRSWLDGSDRGVNTVMQTESFSTGLRCGAFARAGSNYPFD 419
DB 359 NISTFLNPLQTPFRISWLDGSDRGVNTVMQTESFSTGLRCGAFARAGSNYPFD 417
QY 420 YFIRNISGVPLVNERDLRPLHYNEIRNISPSGTRGGLRVMYSVNNRNIVAVHEN 479
DB 418 YFIRNISGVPLVNERDLRPLHYNEIRNISPSGTRGGLRVMYSVNNRNIVAVHEN 471
QY 480 GIMHILAPEDYTGTTTSPPIHATQVNNQTRFISSEKFGNQGDSLRFESQNTTAYTLRNG 539
DB 472 GIMHILAPEDYTGTTTSPPIHATQVNNQTRFISSEKFGNQGDSLRFESQNTTAYTLRNG 531
QY 540 NSYNLYLVSLSLNGSTRITVINGRYTASVNTTNDGNDUNNABRELDIMNANVYASDN 599
DB 532 NSYNLYLVSLSLNGSTRITVINGRYTASVNTTNDGNDUNNABRELDIMNANVYASDN 590
QY 600 TVNPLDINTVFNSTGTFELMNTMVPVNTNLPPIY 632
DB 591 TVNPLDINTVFNSTGTFELMNTMVPVNTNLPPIY 623

RESULT 12
AAU02044 standard; Protein; 625 AA.

AAU02044;
29-AUG-2001 (first entry)
B. thuringiensis toxic crystal protein, CryET73.

Delta endotoxin; Lepidopteran-active; crystal protein; insecticide;
transgenic plant; corn; wheat; soybean; oat; cotton; rice; rye; sorghum;
sugarcane; tomato; tobacco; flax; potato; barley; turf grass;
pasture grass; berry; fruit; legume; vegetable; ornamental plant; shrub;
cactus; tree cell; gypsy moth; looper; tobacco budworm; spruce budworm;
cotton leaf perforator; CryET73.

OS Bacillus thuringiensis.

XX MO200119959-A2.

XX 22-MAR-2001.

XX 13-SEP-2000; 2000MO-US25361.

XX 15-SEP-1999; 99US-0153995.

XX (MONS) MONSANTO CO.

XX Baum JA, Chu C, Donovan WP, Glimmer AJ, Ruper MJ;

XX WPI; 2001-281518/29.

XX N-PSDB; AAS02487.

XX Lepidopteran-active Bacillus thuringiensis delta-endotoxin polypeptides

XX and the polynucleotides that encode them, useful for increasing the

XX insect resistance of plant -

XX Claim 5; Page 163-164; 173pp; English.

The sequence represents a B. thuringiensis Lepidopteran-active
delta-endotoxin, crystal protein CryET73. The lepidopteran-active B.
thuringiensis delta-endotoxin polypeptides may be used as compositions
that are applied to plant crops to protect them from insect damage. The
polynucleotides may be used in the production of transgenic plants that
express the insecticidal polypeptides and consequently have improved
insect resistance compared to non-transformed plants. Monocotyledonous or
dicotyledonous plants may be protected in this way, for example corn,
wheat, soybean, oat, cotton, rice, rye, sorghum, sugarcane, tomato,
tobacco, kapok, flax, potato, barley, turf grass, pasture grass, berry,
fruit, legume, vegetable, ornamental plant, shrub, cactus and/or tree
cell. A wide range of insects (e.g. gypsy moth, looper, tobacco budworm,
cotton leaf perforator and spruce budworm) may be affected by application
of the insecticidal polypeptides (full details given in specification).

Sequence 625 AA;

Query Match 77.9%; Score 2582.5; DB 22; Length 625;
Best Local Similarity 80.7%; Pred. No. 5.3e-200;
Matches 503; Conservative 44; Mismatches 65; Indels 11; Gaps 6;

QY 1 MNVANNGRRTTICADYNNVADHPSEFHSKSLDTIRKEMEMKRTDLSLYVPIVGTSSSF 60
DB 1 MNVANNGRRTTICADYNNVADHPSEFHSKSLDTIRKEMEMKRTDLSLYVPIVGTSSSF 60
QY 61 LKRVGSLVGRKILSELQNLIFPSSGIDLMQELIRATEQPIQRLNADTLGRVNAELAGL 120
DB 61 LKRVGSLVGRKILSELQNLIFPSSGIDLMQELIRATEQPIQRLNADTLGRVNAELAGL 120
QY 121 QANIRENQOVNDFLNPONVPLSTSSVTMMQOLFLNLPQFRVQVQQLLLPLPQA 180
DB 121 QANVAFENRQOVNDFLNPONVPLSTSSVTMMQOLFLNLPQFRVQVQQLLLPLPQA 180
QY 181 ANNHLSFRIDVILNADDEMGISAATLTQNTLYKNTTESNYCINTYQTAARGLNRLHD 240
DB 181 ANNHLSFRIDVILNADDEMGISAATLTQNTLYKNTTESNYCINTYQTAARGLNRLHD 240
QY 241 MLEFRTYELNVEFVYSIMSLFKYQSLVSSGANLYASGSGPQOTQSTQDMPFLYSLF 300
DB 241 MLEFRTYELNVEFVYSIMSLFKYQSLVSSGANLYASGSGPQOTQSTQDMPFLYSLF 300
QY 301 QVNSVYVNLGSGARLTQTPNIGLPGTTTHALLAARVNSGVSIGDGA-AYNNQNF 359
DB 299 QVNSVYVNLGSGARLTQTPNIGLPGTTTHALLAARVNSGVSIGDGA-AYNNQNF 358
QY 360 SCSTFLPPLLPFVRSWLDGSDRGVNTVMQTESFSTGLRCGAFARAGSNYPFD 419
DB 359 NISTFLNPLQTPFRISWLDGSDRGVNTVMQTESFSTGLRCGAFARAGSNYPFD 417
QY 420 YFIRNISGVPLVNERDLRPLHYNEIRNISPSGTRGGLRVMYSVNNRNIVAVHEN 479

Db 418 YFRINISGVVGTISNADLAPLHFNHETIRDI---GTTA--VASLVTYNNRKNITVDTHEN 471
 Qy 480 GTMHLAPEDYTGFTISPIHATOVNNQTRTFISEKFNQSDSLRFGSNTTARVTLRGNG 539
 Db 472 GTMHLAPEDYTGFTISPIHATOVNNQTRTFISEKFNQSDSLRFGSNTTARVTLRGNG 531
 Qy 540 NSNLYLRVSLGNSITRTVINGRVYTSANNVTTNNNDGVNDGAFEDIMGNVVASDN 599
 Db 532 NSNLYLRVSLGNSITRTVINGRVYTSANNVTTNNNDGVNDGAFEDIMGNVVASAN 590
 Qy 600 TNPVLDINTVNSGTQFELNANIM 622
 Db 591 TNPVLDIQVTENDNQFELNANIM 613

RESULT 13

AAP83002 standard; protein; 290 AA.

ID AAP83002 standard; protein; 290 AA.
 XX
 AC AAP83002;
 DT 12-JAN-1991 (first entry)
 DE Sequence of P-2 protein of *Bacillus thuringiensis* var. *kurstaki*.
 XX Insecticide; lepidoptera; diptera; P-2 delta-endotoxin;
 KM parasporal crystal protein.
 XX
 OS *Bacillus thuringiensis*.
 XX
 \$N MO8808034-A.
 PD 20-OCT-1988.
 XX
 PF 07-APR-1988; 88MO-US01132.
 XX
 PR 16-APR-1987; 87US-0039542.
 PA (ECOG-) ECOGEN INC.
 PI Donovan WP;
 DR WPI; 1988-307569/43.
 DR N-PSDB; AAN80591.
 XX
 XX *Bacillus thuringiensis* P-2 toxic gene and expressed protein -
 PT used in insecticidal compns. having activity against
 PT lepidoptera and diptera insects
 XX
 PS Claim 10; Fig 2(1) and Fig 2(3); 66pp; English.
 CC A gene for *Bacillus thuringiensis* (B.t.) P-2 toxin having the DNA
 CC sequence specified in Fig 2 (AAN80591), or any portion or deriv. of it,
 CC is claimed. Also claimed is the protein encoded by the gene, having the
 CC corresponding specified AA sequence in AAP83002. In isolating the P-2
 CC gene, the P-2 protein was purified from a donor strain of B.t. var.
 CC *kurstaki* and the partial AA sequence of the P-2 protein was determined.
 CC P-2 gene-specific oligo probe (AAN80590) was synthesized based on the AA
 CC sequence. The P-2 toxin encoded by the cloned gene has insecticidal
 CC activity against lepidoptera and diptera insects.
 CC N.B. The DNA/protein sequence in AAN80591/P83002 is as given in the
 CC specifications and is missing bases 901-1000 and the corresp. AAs.
 XX
 SQ Sequence 290 AA;

Query Match 38.5%; Score 1274.5; DB 9; Length 290;

Best Local Similarity 46.2%; Pred. No. 1,1e-94;

Matches 271; Conservative 13; Mismatches 3; Indels 299; Gaps 1;

Qy 1 MNVTIANGRRTTICDAVNVVAHDPSFEHKSLLTIRKEMEKRTDHSLLYAPVGTSSSF 60
 Db 1 MNVTIANGRRTTICDAVNVVAHDPSFEHKSLLTIRKEMEKRTDHSLLYAPVGTSSSF 60

Qy 61 LKKVYSLICKRTILSELWGLIFPSGNTLMODILRETEQFLNCHLNTDILARVNALEGL 120
 Db 61 LKKVYSLICKRTILSELWGLIFPSGNTLMODILRETEQFLNCHLNTDILARVNALEGL 120
 Qy 121 QANIREFNOVDNFMNPTONPVPLSTSSVNTMQLFLNRLPQRFVQGLLLPLFPAQA 180
 Db 121 QANIREFNOVDNFMNPTONPVPLSTSSVNTMQLFLNRLPQRFVQGLLLPLFPAQA 180
 Qy 181 ANMHLSPTRDVNANADENGISATLFTYQNYLKNYTESNYVCINTYQTAFFGLNTRLHD 240
 Db 181 ANMHLSPTRDVNANADENGISATLFTYQNYLKNYTESNYVCINTYQTAFFGLNTRLHD 240
 Qy 241 MLEFRTYVPLNVEEYVSWLSLFTQSLVSSGANLYAGSGPQOTQSTFSQMPPLVSLF 300
 Db 241 MLEFRTYVPLNVEEYVSWLSLFTQSLVSSGANLYAGSGPQOTQSTFSQMPPLVSLF 300
 Qy 301 QVNSNYVLNGPSGARLTQTFPNIGLPGTTTHALLAARVNSGVSSGPDIGAVRNQNS 360
 Db 249 ----- 248
 Qy 361 CSTPLPLLPFVRSWLDGSDRGVNTVNTMOTESFESTGLACGAFARGNSNPPDY 420
 Db 249 ----- 248
 Qy 421 FTRINISGVPLVNEREDLRPLHYEININIESPSGTGGLRAVMSVNRKNITVAVHENG 480
 Db 249 ----- 248
 Qy 481 TMIHLAPEDYTGFTISPIHATOVNNQTRTFISEKFNQSDSLRFGSNTTARVTLRGNG 540
 Db 249 ----- 248
 Qy 541 SYNLYLRVSLGNSITRTVINGRVYTSANNVTTNNNDGVNDGAF 586
 Db 249 -----LSIGNSTIRVTINGRVYTSANNVTTNNNDGVNDGAF 287

RESULT 14

AAM31199 standard; Protein; 706 AA.

ID AAM31199 standard; Protein; 706 AA.
 XX
 AC AAM31199;
 DT 13-FEB-1998 (first entry)
 DE *Bacillus popilliae* crystal protein.
 XX
 KM Crystal protein; beetle; Scarabaeidae; maybug; cockchafer;
 KM agricultural pest; spore; *Bacillus thuringiensis*; cytolysing protein;
 KM fusion protein; transgenic plant.
 XX
 OS *Bacillus popilliae*.
 FH Key
 FT Protein
 FT Location/Qualifiers
 FT 1..706
 FT /label= crystal protein
 PN DEL19642729-A1.
 PD 24-APR-1997.
 PF 17-OCT-1996; 96DE-1042729.
 PR 18-OCT-1995; 95DE-1040223.
 PA (UYHE-) UNIT HEIDELBERG.
 PI Krieger L, Schmetter W, Zhang J;
 DR WPI; 1997-237512/22.
 DR N-PSDB; AAT89348.
 XX

PT DNA encoding *Bacillus popilliae* crystal protein - for production of
 PT recombinant protein and transgenic plants resistant to attack by
 beetles

XX Claim 8; Pages 8-11; 12pp; German.

XX This sequence represents a novel bacterial crystal protein which can be
 CC used to control beetles of the family Scarabaeidae, especially
 CC *Melolontha* spp. (e.g., maybugs, cockchafer) which are pests of
 CC agriculture and forestry. The protein can inhibit eating, killing both
 CC adult beetles and larvae. It can be incorporated into eradication
 CC programmes involving *Bacillus popilliae* and *Bacillus thuringiensis*
 CC spores, fungal spores or cyclolyzing proteins in the form of a fusion
 CC protein. The DNA can also be used to produce transgenic plants that are
 CC resistant to attack by the beetles.

XX Sequence 706 AA.

Query Match 32.6%; Score 1082; DB 18; Length 706;
 Best Local Similarity 38.6%; Pred. No. 1.5e-79;
 Matches 265; Conservative 95; Mismatches 233; Indels 94; Gaps 21.

QY 2 NNVLAN-----GRITICDA-----YNAVHDPSPFHKSLDTIKEMEMKRTD 45
 DB 58 NNDNNNDACIDELGIPIDNNITICSTDPINVRDPP--FKKSTOELTREMTEWKNES 115
 QY 46 HSLVAVPIVGVTSFLIKKVGSLIKRILSELWGLIFPSGSNTLMODILRETEQFQRL 105
 DB 116 PSILFTPAIVGVVTSFLLOSILKQATSLFKTLTLIFPNNSLSLMEILRATQGYOERL 175
 QY 106 NNDTLARVNAELGLQANIREFNOQVDFNFPQNPVPISTSSNTMCOQLFNLRLPQR 165
 DB 176 DDTIANRVSQELVGLKNNLTTRNDYEDFQLNKGVSPLAIDISINTMOQLFNLRLPQR 235
 QY 166 VGGIQLLLPLFAQANMHLSTRDVYNADWGISAAATLRTYQYLNKNTTYSNYCIN 225
 DB 236 VSGYQVLLPLFAQANMHLSTRDVYNADWGISAAATLRTYQYLNKNTTYSNYCIN 295
 QY 226 TYQTAFRGANTR-----LADMLEPRTMFLNFEVYSIWSLFKYGSLVSGANIXASG 279
 DB 296 TYDGEFR---TRFYPNTLEDLQKPTMTLMDLVSIWSLKIYMLVSTANLYNIG 352
 QY 280 SGPQOTOSTSQMPLFYLFPVNSNYLNGFSGARLTQTFENIG-----LPQTTTTH 333
 DB 353 DNKVNAGYPISYGPFENSYIQVKSNNYVLSGVSGIGARPTSYVLGRLHDLKNIIT- 411
 QY 334 ALLARVYSGVSGDIGAVFN-----ONFSCSTFLP-PLTLP 371
 DB 412 -----YVGTOGNIIGVQLSTTEDELKQOQATRDSLVDFQFTLNCMLPENITAP 463
 QY 372 -FVSMWLDSC-SDRGAVNTVNNQTESFESTLGL-RCGAFTARGNSYPPDYFIRINISGV 428
 DB 464 YFATSLVESRYSSIGGYLKKDVFKE--DSTCLGPNGAMTS-----YDYIYNISAT 515
 QY 429 PLVANNEDLRPLAHYIEINIESPSGPGGLRAYVWSVYNNRNINIVAHNGMHLAPE 488
 DB 516 VQINGEMTDTPLYFENRPISTRGV-----NKVAYVNRKANIACTONGMTHQAP 570
 QY 489 DYTGTISPIHATQVNNQTRTFISKFGQSDSLREDSNTTAYTLRNG-NSYNLYLR 547
 DB 571 DGTGTVSPHPSA--NITTSYIKENYNGSDSLHL-KQGYLHMYLSGQDRRLVLR 627
 QY 548 VSLGNGSTIRVTINGEYVYASVNTTNNQDVNDGAPFLINNGN--VVASDNNNVPLD 605
 DB 628 LSGAAN---QIKQSPTSIYAFDSTINNGITDNGSKFKDPAFSTFVPIBOK-----E 679
 QY 606 INTFNSGTQFELAMINMFVNNLPPIY 632
 DB 680 IVLTFBGVSLDMLNLIPLADDTPLY 706

RESULT 15
 AAP81356

ID AAP81356 standard; protein; 99 AA.

XX AAP81356;

AC 12-JUN-1991 (first entry)

DE Sequence of fragment of *Bacillus thuringiensis* P-2 protein.

KW Insecticide; lepidoptera; diptera; P-2 delta-endotoxin;

KW parasporal crystal protein.

OS *Bacillus thuringiensis*.

FN W08808034-A.

PD 20-OCT-1988.

PF 07-APR-1988; 68WC-US01132.

PR 16-APR-1987; 67US-0039542.

PA (ECOG-) ECOGEN INC.

PI Donovan WP;

DR WPI; 1988-307569/43.

PT *Bacillus thuringiensis* P-2 toxin gene and expressed protein -

PT used in insecticidal compns. having activity against

PT lepidoptera and diptera insects

PS Claim 73; Fig 6 and Page 54; 66pp; English.

XX A gene for *Bacillus thuringiensis* (B.t.) P-2 toxin having the DNA
 CC sequence specified in Fig 2 (AAN80591), or any portion or deriv. of it,
 CC is claimed. Also claimed is the protein encoded by the gene, having the
 CC corresponding specified AA sequence in AAN80546. In isolating the P-2
 CC gene, the P-2 protein was purified from a donor strain of B.t. var.
 CC kurstaki and the partial AA sequence of the P-2 protein was determined.
 CC P-2 gene-specific oligo probe (AAN80590) was synthesised based on the
 CC sequence. The P-2 toxin encoded by the cloned gene has insecticidal
 CC activity against lepidoptera and diptera insects. SQ corresponds to
 CC residues 162-260 of the P-2 protein.

XX Sequence 99 AA;

Query Match 15.1%; Score 499; DB 9; Length 99;

Best Local Similarity 91.9%; Pred. No. 1.2e-32;

Matches 91; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

QY 162 PQPRVGGYQLLLPLFAQANMHLSTRDVYNADWGISAAATLRTYQYLNKNTTYSN 221

DB 1 PQPRVGGYQLLLPLFAQANMHLSTRDVYNADWGISAAATLRTYQYLNKNTTYSN 60

QY 222 YCINTYQTAFRGLNTRLDMLERRTYMFLNFEVYSIWS 260

DB 61 YCINTYQTAFRGLNTRLDMLERRTYMFLNFEVYSIWS 99

Search completed: August 14, 2003, 18:11:01

Job time : 53 secs

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•
•

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OM protein - protein search, using sw model

Run on: August 14, 2003, 18:10:07 ; Search time 30 Seconds
(without alignments)
891.349 Million cell updates/sec

Title: US-10-040-906a-2

Perfect score: 3314
Sequence: 1 MNVYNGRTTICDANYVVA.....GTPELKNIMFVTLPEPY 632

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: /cg2_6/ptodata/1/aa/5A.COMB.pep.*
2: /cg2_6/ptodata/1/aa/5B.COMB.pep.*
3: /cg2_6/ptodata/1/aa/5A.COMB.pep.*
4: /cg2_6/ptodata/1/aa/5B.COMB.pep.*
5: /cg2_6/ptodata/1/aa/5A.COMB.pep.*
6: /cg2_6/ptodata/1/aa/5B.COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3043.5	91.8	634	US-09-186-002-12	Sequence 12, Appl
2	3015.5	91.0	635	US-09-041-991A-4	Sequence 4, Appl
3	3015.5	91.0	635	US-09-608-533A-4	Sequence 4, Appl
4	3015.5	90.8	633	US-09-186-002-18	Sequence 18, Appl
5	3005.5	90.7	634	US-09-186-002-2	Sequence 2, Appl
6	2914.5	87.9	633	US-09-041-991A-10	Sequence 10, Appl
7	2914.5	87.9	633	US-09-608-533A-10	Sequence 10, Appl
8	2913.5	87.9	633	US-09-041-991A-8	Sequence 8, Appl
9	2913.5	87.9	633	US-09-608-533A-8	Sequence 8, Appl
10	2610.5	78.8	623	US-09-041-991A-6	Sequence 6, Appl
11	2610.5	78.8	623	US-09-608-533A-6	Sequence 6, Appl
12	1080	32.6	706	US-09-408-820-2	Sequence 2, Appl
13	336.5	10.2	644	US-08-793-331-7	Sequence 7, Appl
14	327.5	9.9	648	US-08-286-870A-4	Sequence 4, Appl
15	327.5	9.9	719	US-08-286-870A-8	Sequence 8, Appl
16	311.5	9.4	1156	US-09-002-285-72	Sequence 72, Appl
17	311.5	9.4	1156	US-09-589-477-72	Sequence 72, Appl
18	307	9.3	1157	US-08-532-547-5	Sequence 5, Appl
19	307	9.3	1157	US-08-379-6568-5	Sequence 5, Appl
20	307	9.3	1157	US-08-455-838-5	Sequence 5, Appl
21	307	9.3	1157	US-09-019-809-9	Sequence 9, Appl
22	307	9.3	1157	US-09-471-177-7	Sequence 7, Appl
23	306	9.2	1138	US-07-973-320-4	Sequence 4, Appl
24	306	9.2	1138	US-07-973-320-4	Sequence 4, Appl
25	305.5	9.2	1186	US-09-178-252-23	Sequence 23, Appl
26	305.5	9.2	1186	US-09-178-252-23	Sequence 23, Appl
27	305.5	9.2	1227	US-08-448-170-8	Sequence 8, Appl

28	305.5	9.2	1227	US-08-361-803-9	Sequence 9, Appl
29	304.5	9.2	625	US-08-532-547-7	Sequence 7, Appl
30	304.5	9.2	625	US-08-532-547-9	Sequence 9, Appl
31	304.5	9.2	625	US-09-019-809-7	Sequence 7, Appl
32	304.5	9.2	625	US-09-019-809-9	Sequence 9, Appl
33	304.5	9.2	625	US-09-471-177-7	Sequence 7, Appl
34	304.5	9.2	625	US-09-471-177-9	Sequence 9, Appl
35	294.5	8.9	1176	US-08-434-823-2	Sequence 2, Appl
36	294.5	8.9	1176	US-08-457-368-2	Sequence 2, Appl
37	293.5	8.9	1229	US-08-100-709-4	Sequence 4, Appl
38	293.5	8.9	1229	US-08-176-865-4	Sequence 4, Appl
39	293.5	8.9	1229	US-08-474-038-4	Sequence 4, Appl
40	293.5	8.9	1229	US-08-779-046-4	Sequence 4, Appl
41	293.5	8.9	1229	US-08-881-340-4	Sequence 4, Appl
42	292	8.8	488	US-08-448-170-10	Sequence 10, Appl
43	292	8.8	488	US-08-961-803-10	Sequence 10, Appl
44	291.5	8.8	1179	US-08-040-751-1	Sequence 1, Appl
45	288.5	8.7	1176	US-07-828-788A-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-09-186-002-12
Sequence 12, Application US/091860028
Patent No. 6489542
GENERAL INFORMATION:
APPLICANT: Corbin, David R.
APPLICANT: Romano, Charles P.
TITLE OF INVENTION: Improved Method for Transforming Plants to Express
FILE REFERENCE: 38-21(13547) US Pat No. 6489542 09/186,002
CURRENT APPLICATION NUMBER: US/09/186,0028
CURRENT FILING DATE: 1998-11-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 12
LENGTH: 634
TYPE: PRT
ORGANISM: Bacillus thuringiensis
US-09-186-002-12

Query Match	91.8%	Score 3043.5	DB 4	Length 634
Best Local Similarity	90.7%	Pred. No. 1.4e-262		
Matches 573	Conservative 34	Mismatches 24	Indels 1	Gaps 1
QY	2	NNVYNGRTTICDANYVVAHDPFSEHKSIDTIRKEMEMKRTDHSLYVAPITGVSSFL	61	
DB	3	NNVYNGRTTICDANYVVAHDPFSEHKSIDTIRKEMEMKRTDHSLYVAPITGVSSFL	62	
QY	62	LKVGSLIGRIISLSEMLIPSSSTLMODILIRETEOFLNORLNTDTLARVAELISGL	121	
DB	63	LKVGSLIGRIISLSEMLIPSSSTLMODILIRETEOFLNORLNTDTLARVAELISGL	122	
QY	122	ANIREFOQVDFNLFQNPVPLSITSSVTMOQLFLNRLPQFVQGYQLLPLFAQA	181	
DB	123	ANIREFOQVDFNLFQNPVPLSITSSVTMOQLFLNRLPQFVQGYQLLPLFAQA	182	
QY	182	NMHSFIRVDVLAADKMSAATRTQNLKNTTETRSNCTINTTQAFRLRLHDM	241	
DB	183	NMHSFIRVDVLAADKMSAATRTQNLKNTTETRSNCTINTTQAFRLRLHDM	242	
QY	242	LEFRTYFLNVEFYVIMSLFKYQSLVSGANLYASGSGPQOTGFTSQDMPFLYSFQ	301	
DB	243	LEFRTYFLNVEFYVIMSLFKYQSLVSGANLYASGSGPQOTGFTSQDMPFLYSFQ	302	
QY	302	VNSVYVANGSGARLTOFEPNIGSLPCTTHALLAARVYSGVSSGIDYAV-FNONS	360	
DB	303	VNSVYVANGSGARLTOFEPNIGSLPCTTHALLAARVYSGVSSGIDYAV-FNONS	362	
QY	361	CSTLPPLTPVRSWMDSGSDRGVYVTVNMQTESPSTGLRCAPFARNGSNYPEDY	420	

Db 363 CSTVLPPLSTPFVRSMDSGTDRGVATSTNNQTESFOTLISLRCAFSARNSNPPDY 422
QY 421 FIRMISGVPLVRNEDLRPLHYNEIRNIESPSGTGGRLAYVSVHNRKNNTYAVHENG 480
Db 423 FIRMISGVPLVRNEDLRPLHYNQIRNIESPSGTGGRLAYVSVHNRKNNTYAVHENG 482
QY 481 TMTLAPEDYGTFTSPHATQVNNQTRFISEKFGNQSGLFPEQSNTTARVTLRNGN 540
Db 483 TMTLAPEDYGTFTSPHATQVNNQTRFISEKFGNQSGLFPEQSNTTARVTLRNGN 542
QY 541 SYNTLVSSISAGNSTRTYINGRVYVTSNVNTTNNDSVNDGNGARFLDINNCGVAVSDNT 600
Db 543 SYNTLVSSISAGNSTRTYINGRVYVTSNVNTTNNDSVNDGNGARFLDINNCGVAVSDNT 602
QY 601 NVPLDINVTPNSGTQFELNMIMFVPTNLPPLY 632
Db 603 NVPLDINVTPNSGTQFELNMIMFVPTNLPPLY 634

RESULT 2

US-09-041-991A-4
Sequence 4, Application US/09041991A
Patent No. 6107278
GENERAL INFORMATION:
APPLICANT: Schepf, H. Ernest
APPLICANT: Narva, Kenneth E.
APPLICANT: Muller-Cohn, Judy
TITLE OF INVENTION: Toxins Active Against Pests
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,991A
CLASSIFICATION: 514
FILING DATE: 13-MAR-1998
ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-709
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 635 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-041-991A-4

Query Match 91.0%; Score 3015.5; DB 3; Length 635;
Best Local Similarity 90.2%; Pred. No. 4.3e-260;
Matches 573; Conservative 30; Mismatches 29; Indels 3; Gaps 2;
QY 1 MNVNLNGRTTICDQVYVVAHDPFSEHKSDITRKEMWEMKRTDHSIYVAPIVGVSSF 60
Db 1 MNVNLNGRTTICDQVYVVAHDPFSEHKSDITRKEMWEMKRTDHSIYVAPIVGVSSF 60
QY 61 LKKVGSLLIGRIILSELMGLIFPSSGSTNLMODILRETEQVLANRANTTTTLARVNALEEG 120
Db 61 LKKVGSLLIGRIILSELMGLIFPSSGSTNLMODILRETEQVLANRANTTTTLARVNALEEG 120

QY 121 QANIREFNOQVDNLFNPTQNPVPLSTTSVNTMOQLFLNRLPQFQIOGYQLLLPLFQA 180
Db 121 QANIREFNOQVDNLFNPTQNPVPLSTTSVNTMOQLFLNRLPQFQIOGYQLLLPLFQA 180
QY 181 ANNHLSFTRDVLNADWEGISAATLRTYQNTLKYNTTESVNCINTYQTFRGLNRLHD 240
Db 181 ANNHLSFTRDVLNADWEGISAATLRTYQNTLKYNTTESVNCINTYQTFRGLNRLHD 240
QY 241 MLEFRTYMLNVEFEYYSIMSLFKYQSLVSSGANLYASGSGPQOTQSFSDWPELYSLF 300
Db 241 MLEFRTYMLNVEFEYYSIMSLFKYQSLVSSGANLYASGSGPQOTQSFSDWPELYSLF 300
QY 301 QVNSVYVNLGSSGKRLQTFPPNIGLPGTTTHALLAARVNSGGVSGDYGAV-ENQRF 359
Db 301 QVNSVYVNLGSSGKRLQTFPPNIGLPGTTTHALLAARVNSGGVSGDYGAV-ENQRF 360
QY 360 SCSTFLPPLTPFVRSMDSGTDRGVNTVNNQTESFESTLGLRCA--FTARGNSNF 417
Db 361 NCSTVLPPLSTPFVRSMDSGTDRGVATSTNNQTESFOTLISLRCAFPFSARNSNPF 420
QY 418 PDYFIRNISGVPLVRNEDLRPLHYNEIRNIESPSGTGGRLAYVSVHNRKNNTYAVH 477
Db 421 PDYFIRNISGVPLVRNEDLRPLHYNQIRNIESPSGTGGRLAYVSVHNRKNNTYAVH 480
QY 478 ENGTMTHLAPEDYGTFTSPHATQVNNQTRFISEKFGNQSGLFPEQSNTTARVTLRNG 537
Db 481 ENGTMTHLAPEDYGTFTSPHATQVNNQTRFISEKFGNQSGLFPEQSNTTARVTLRNG 540
QY 538 NGNSVYVNLGSSGKRLQTFPPNIGLPGTTTHALLAARVNSGGVSGDYGAV-ENQRF 597
Db 541 NGNSVYVNLGSSGKRLQTFPPNIGLPGTTTHALLAARVNSGGVSGDYGAV-ENQRF 600
QY 598 DNTNVPDLINVTPNSGTQFELNMIMFVPTNLPPLY 632
Db 601 DNTNVPDLINVTPNSGTQFELNMIMFVPTNLPPLY 635

RESULT 3

US-09-608-533A-4
Sequence 4, Application US/09608533A
Patent No. 653464
GENERAL INFORMATION:
APPLICANT: Schepf, H. Ernest
APPLICANT: Narva, Kenneth E.
APPLICANT: Muller-Cohn, Judy
TITLE OF INVENTION: Toxins Active Against Pests
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/608,533A
FILING DATE: 30-Jun-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/041,991
FILING DATE: 13-MAR-1998
ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-709D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 635 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-09-608-533A-4

Query Match 91.0%; Score 3015.5; DB 4; Length 635;
Best Local Similarity 90.2%; Pred. No. 4,3e-260;

Matches 573; Conservative 30; Mismatches 29; Indels 3; Gaps 2;

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QY 1 MNNVANNGRITTCDAVYVVAADPFSEHKSIDITRKEMEMKRTDHSYVAVIGTVSSP 60
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Db 1 MNNVANNGRITTCDAVYVVAADPFSEHKSIDITRKEMEMKRTDHSYVAVIGTVSSP 60
QY 61 LKKVSLIGKRILSELWGLIFPSGSTNLMODILRETEQFLNORLNTDTLARVAELEG 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 LKKVSLIGKRILSELWGLIFPSGSTNLMODILRETEQFLNORLNTDTLARVAELEG 120
QY 121 QANIREFNOQVDNPLNPNPVPPLSTSSVNTMOQLFNLRLPQFVQGYQLLLPLPAQA 180
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 121 QANIREFNOQVDNPLNPNPVPPLSTSSVNTMOQLFNLRLPQFVQGYQLLLPLPAQA 180
QY 181 ANHLSFIRDVILNADWEGISAATLRTYQNYLKNYTESYNCINTYQTAFFGLNTRLHD 240
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Db 181 ANHLSFIRDVILNADWEGISAATLRTYQNYLKNYTESYNCINTYQTAFFGLNTRLHD 240
QY 241 MLEFRTYMFANFEYVSIWLSFKYQSLVSSGANLYASGSGPOQTOSFTSQDMPPLYSLF 300
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 241 MLEFRTYMFANFEYVSIWLSFKYQSLVSSGANLYASGSGPOQTOSFTSQDMPPLYSLF 300
QY 301 QVNSNVYLVNGFSGARLVTQFPNIGLPETTTTHALLAARVNSGVSAGDIGA- FNONF 359
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 301 QVNSNVYLVNGFSGARLVTQFPNIGLPETTTTHALLAARVNSGVSAGDIGA- FNONF 359
QY 360 SCSTFLPPLLPFPVSWLDSGDRGVNTVNTMOTESPESTGLRGA- FTAAGNNTYF 417
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 360 SCSTFLPPLLPFPVSWLDSGDRGVNTVNTMOTESPESTGLRGA- FTAAGNNTYF 417
QY 421 PDYFIRNISGVPLVVRNEDLRPLAYNEIRNIESPSGTPGGLRAYVSVHNRKNNIYAVH 477
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Db 421 PDYFIRNISGVPLVVRNEDLRPLAYNEIRNIESPSGTPGGLRAYVSVHNRKNNIYAVH 477
QY 478 ENGTMILAPEDYGTFTSPIHATOVNNOQRTFISEKFGQGSILRFEOSNTTARTYLRKG 537
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Db 478 ENGTMILAPEDYGTFTSPIHATOVNNOQRTFISEKFGQGSILRFEOSNTTARTYLRKG 537
QY 538 NGNSVYLKRVSSLSGNSTIRVTINGRVTYASVNTTNDGVNDGARFLDINMGVVAS 597
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Db 538 NGNSVYLKRVSSLSGNSTIRVTINGRVTYASVNTTNDGVNDGARFLDINMGVVAS 597
QY 541 NGNSVYLKRVSSLSGNSTIRVTINGRVTYASVNTTNDGVNDGARFLDINMGVVAS 600
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 541 NGNSVYLKRVSSLSGNSTIRVTINGRVTYASVNTTNDGVNDGARFLDINMGVVAS 600
QY 598 DNTNVPDLINVTNSGTQFELMNTMVPNTNLPY 632
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 598 DNTNVPDLINVTNSGTQFELMNTMVPNTNLPY 632
QY 601 DNTNVPDLINVTNSGTQFELMNTMVPNTNLPY 635
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 601 DNTNVPDLINVTNSGTQFELMNTMVPNTNLPY 635

```

RESULT 4
US-09-186-002-18
Sequence 18, Application US/09186002B
Patent No. 6489542
GENERAL INFORMATION:
APPLICANT: Corbin, David R.
APPLICANT: Romano, Charles P.
TITLE OF INVENTION: Improved Method for Transforming Plants to Express
FILE REFERENCE: 38-21(13547) US Pat No. 6489542 09/186,002
CURRENT FILING DATE: 1998-11-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 18
LENGTH: 633
TYPE: PRT
ORGANISM: Bacillus thuringiensis
US-09-186-002-18

Query Match 90.8%; Score 3010.5; DB 4; Length 633;
Best Local Similarity 89.7%; Pred. No. 1.2e-259;
Matches 568; Conservative 39; Mismatches 25; Indels 1; Gaps 1;

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QY 1 MNNVANNGRITTCDAVYVVAADPFSEHKSIDITRKEMEMKRTDHSYVAVIGTVSSP 60
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Db 1 MNNVANNGRITTCDAVYVVAADPFSEHKSIDITRKEMEMKRTDHSYVAVIGTVSSP 60
QY 61 LKKVSLIGKRILSELWGLIFPSGSTNLMODILRETEQFLNORLNTDTLARVAELEG 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 LKKVSLIGKRILSELWGLIFPSGSTNLMODILRETEQFLNORLNTDTLARVAELEG 120
QY 121 QANIREFNOQVDNPLNPNPVPPLSTSSVNTMOQLFNLRLPQFVQGYQLLLPLPAQA 180
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 121 QANIREFNOQVDNPLNPNPVPPLSTSSVNTMOQLFNLRLPQFVQGYQLLLPLPAQA 180
QY 181 ANHLSFIRDVILNADWEGISAATLRTYQNYLKNYTESYNCINTYQTAFFGLNTRLHD 240
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QY 241 MLEFRTYMFANFEYVSIWLSFKYQSLVSSGANLYASGSGPOQTOSFTSQDMPPLYSLF 300
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 241 MLEFRTYMFANFEYVSIWLSFKYQSLVSSGANLYASGSGPOQTOSFTSQDMPPLYSLF 300
QY 301 QVNSNVYLVNGFSGARLVTQFPNIGLPETTTTHALLAARVNSGVSAGDIGA- FNONF 359
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 301 QVNSNVYLVNGFSGARLVTQFPNIGLPETTTTHALLAARVNSGVSAGDIGA- FNONF 359
QY 360 SCSTFLPPLLPFPVSWLDSGDRGVNTVNTMOTESPESTGLRGA- FTAAGNNTYF 419
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 360 SCSTFLPPLLPFPVSWLDSGDRGVNTVNTMOTESPESTGLRGA- FTAAGNNTYF 419
QY 421 YFIRNISGVPLVVRNEDLRPLAYNEIRNIESPSGTPGGLRAYVSVHNRKNNIYAVH 479
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 421 YFIRNISGVPLVVRNEDLRPLAYNEIRNIESPSGTPGGLRAYVSVHNRKNNIYAVH 479
QY 480 GNMILAPEDYGTFTSPIHATOVNNOQRTFISEKFGQGSILRFEOSNTTARTYLRKG 539
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 480 GNMILAPEDYGTFTSPIHATOVNNOQRTFISEKFGQGSILRFEOSNTTARTYLRKG 539
QY 540 NSYNLYRVSSLSGNSTIRVTINGRVTYASVNTTNDGVNDGARFLDINMGVVAS 599
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 540 NSYNLYRVSSLSGNSTIRVTINGRVTYASVNTTNDGVNDGARFLDINMGVVAS 599
QY 600 TVVPLDINVTNSGTQFELMNTMVPNTNLPY 632
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 600 TVVPLDINVTNSGTQFELMNTMVPNTNLPY 632
QY 601 SDVPLDINVTNSGTQFELMNTMVPNTNLPY 633
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 601 SDVPLDINVTNSGTQFELMNTMVPNTNLPY 633

```

RESULT 5
US-09-186-002-2
Sequence 2, Application US/09186002B
Patent No. 6489542
GENERAL INFORMATION:
APPLICANT: Corbin, David R.
APPLICANT: Romano, Charles P.
TITLE OF INVENTION: Improved Method for Transforming Plants to Express
FILE REFERENCE: 38-21(13547) US Pat No. 6489542 09/186,002
CURRENT FILING DATE: 1998-11-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 634
TYPE: PRT
ORGANISM: Bacillus thuringiensis

Fri Aug 15 11:51:34 2003

us-10-040-906a-2.rat

Page 4

US-09-186-002-2

Query Match 90.7%; Score 3005.5; DB 4; Length 634;
Best Local Similarity 89.7%; Pred. No. 3.3e-259;
Matches 567; Conservative 39; Mismatches 25; Indels 1; Gaps 1;

QY 2 NNVLNNGRTTICDANNVVAHDPFSEHKSIDTIRKEMEMKRDHSLYVAPVIGVYSSFL 61
DB 3 NSVNSGRRTTICDANNVVAHDPFSEHKSIDTIRKEMEMKRDHSLYVAPVIGVYSSFL 62
QY 62 LKKGSLIGKRIISLSEIMGLIPPSGNTLMODILRETEFOPLNORLNTDTLLARVNAELGQ 121
DB 63 LKKGSLIGKRIISLSEIMGLIPPSGNTLMODILRETEFOPLNORLNTDTLLARVNAELGQ 122
QY 122 ANIREFOQVDFNPLNPTONPVPISITSSVNTMOQLFLNRLPOFVQOYQLLLPLFAQA 181
DB 123 ANIREFOQVDFNPLNPTONPVPISITSSVNTMOQLFLNRLPOFVQOYQLLLPLFAQA 182
QY 182 NMHLSPTRDVLNADDEMGISAATLRTYQNYLKNYTESNYCINTYQTAERGLNTRLHD 241
DB 183 NMHLSPTRDVLNADDEMGISAATLRTYQNYLKNYTESNYCINTYQTAERGLNTRLHD 242
QY 242 LEFRTYMLNVEFYVWSLFRYQSLVSSGANLVASGSGPOQOSFTSQDMPFLYSLFQ 301
DB 243 LEFRTYMLNVEFYVWSLFRYQSLVSSGANLVASGSGPOQOSFTSQDMPFLYSLFQ 302
QY 302 VNSNVYVNGFSGARLTQTFPNIGLPGTTTHALLAARVNSGVVSGDI GA-VNPNQFS 360
DB 303 VNSNVYVNGFSGARLTQTFPNIGLPGTTTHALLAARVNSGVVSGDI GA-VNPNQFS 362
QY 361 CSTFLPPLITPFRVSWLDSGDRGVNTVMQTESFESTTGLRCGAFARAGNSNFPDY 420
DB 363 CSTFLPPLITPFRVSWLDSGDRGVNTVMQTESFESTTGLRCGAFARAGNSNFPDY 422
QY 421 FTRNIGVPLVVRNEDLRPLHYNEIRNIESPGTCGRLAAMVSYNRKNNTYVHNG 480
DB 423 FTRNIGVPLVVRNEDLRPLHYNEIRNIESPGTCGRLAAMVSYNRKNNTYVHNG 482
QY 481 TWIHLAPEDYGTFTSPIHATOVNQTFTPISEFGQSDSLRFGOSNTTARATLKGNG 540
DB 483 TWIHLAPEDYGTFTSPIHATOVNQTFTPISEFGQSDSLRFGOSNTTARATLKGNG 542
QY 541 SYNLYLRVSSLSGNTIRVTINGRVYTAASVNTTNDGVNDGARFDLIMNGVVASDN 600
DB 543 SYNLYLRVSSLSGNTIRVTINGRVYTAASVNTTNDGVNDGARFDLIMNGVVASDN 602
QY 601 NVPLDINTVNSGTQFELNMIMFVPTNLPLY 632
DB 603 NVPLDINTVNSGTQFELNMIMFVPTNLPLY 634

RESULT 6
US-09-041-991A-10
Sequence 10, Application US/09041991A
Patent No. 6107278

GENERAL INFORMATION:
APPLICANT: Schepf, H. Ernest
APPLICANT: Narva, Kenneth E.
APPLICANT: Miller-Cohn, Judy
TITLE OF INVENTION: Toxins Active Against Pests
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,991A
FILING DATE: 13-MAR-1998
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-709
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 633 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-041-991A-10

Query Match 87.9%; Score 2914.5; DB 3; Length 633;
Best Local Similarity 87.0%; Pred. No. 4.3e-251;
Matches 551; Conservative 44; Mismatches 37; Indels 1; Gaps 1;

QY 1 MNVNLNNGRTTICDANNVVAHDPFSEHKSIDTIRKEMEMKRDHSLYVAPVIGVYSSFL 60
DB 1 MNVNLNNGRTTICDANNVVAHDPFSEHKSIDTIRKEMEMKRDHSLYVAPVIGVYSSFL 60
QY 61 LKKGSLIGKRIISLSEIMGLIPPSGNTLMODILRETEFOPLNORLNTDTLLARVNAELGQ 120
DB 61 LKKGSLIGKRIISLSEIMGLIPPSGNTLMODILRETEFOPLNORLNTDTLLARVNAELGQ 120
QY 121 QANIREFOQVDFNPLNPTONPVPISITSSVNTMOQLFLNRLPOFVQOYQLLLPLFAQA 180
DB 121 QANIREFOQVDFNPLNPTONPVPISITSSVNTMOQLFLNRLPOFVQOYQLLLPLFAQA 180
QY 181 NMHLSPTRDVLNADDEMGISAATLRTYQNYLKNYTESNYCINTYQTAERGLNTRLHD 240
DB 181 NMHLSPTRDVLNADDEMGISAATLRTYQNYLKNYTESNYCINTYQTAERGLNTRLHD 240
QY 241 MLEFRTYMLNVEFYVWSLFRYQSLVSSGANLVASGSGPOQOSFTSQDMPFLYSLF 300
DB 241 MLEFRTYMLNVEFYVWSLFRYQSLVSSGANLVASGSGPOQOSFTSQDMPFLYSLF 300
QY 301 QVNSNVYVNGFSGARLTQTFPNIGLPGTTTHALLAARVNSGVVSGDI GA-VNPNQFS 360
DB 301 QVNSNVYVNGFSGARLTQTFPNIGLPGTTTHALLAARVNSGVVSGDI GA-VNPNQFS 360
QY 360 SCSTFLPPLITPFRVSWLDSGDRGVNTVMQTESFESTTGLRCGAFARAGNSNFPDY 419
DB 361 SCSTFLPPLITPFRVSWLDSGDRGVNTVMQTESFESTTGLRCGAFARAGNSNFPDY 420
QY 420 YFIRNIGVPLVVRNEDLRPLHYNEIRNIESPGTCGRLAAMVSYNRKNNTYVHNG 479
DB 421 YFIRNIGVPLVVRNEDLRPLHYNEIRNIESPGTCGRLAAMVSYNRKNNTYVHNG 480
QY 480 GTWHLAPEDYGTFTSPIHATOVNQTFTPISEFGQSDSLRFGOSNTTARATLKGNG 539
DB 481 GTWHLAPEDYGTFTSPIHATOVNQTFTPISEFGQSDSLRFGOSNTTARATLKGNG 540
QY 540 NSYNYLRVSSLSGNTIRVTINGRVYTAASVNTTNDGVNDGARFDLIMNGVVASDN 599
DB 541 NSYNYLRVSSLSGNTIRVTINGRVYTAASVNTTNDGVNDGARFDLIMNGVVASDN 600
QY 600 NVPLDINTVNSGTQFELNMIMFVPTNLPLY 632
DB 601 NVPLDINTVNSGTQFELNMIMFVPTNLPLY 633

RESULT 7
US-09-608-533A-10
Sequence 10, Application US/09608533A
Patent No. 6534644

GENERAL INFORMATION:

APPLICANT: Schnepf, H. Ernest
 Narva, Kenneth E.
 Muller-Cohn, Judy

TITLE OF INVENTION: Toxins Active Against Peets

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
 STREET: 2421 N.W. 41st Street, Suite A-1
 CITY: Gainesville
 STATE: Florida
 COUNTRY: USA
 ZIP: 32606

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/608,533A
 FILING DATE: 30-Jun-2000
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 09/041,991
 FILING DATE: 13-MARCH-1998

ATTORNEY/AGENT INFORMATION:
 NAME: Sanders, Jay M.
 REGISTRATION NUMBER: 39,355
 REFERENCE/DOCKET NUMBER: MA-709D1

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (352) 375-8100
 TELEFAX: (352) 372-5800

INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 633 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 10:
 US-09-608-533A-10

Query Match

Best Local Similarity 87.9%; Score 2914.5; DB 4; Length 633;
 Matches 551; Conservatve 44; Mismatches 37; Indels 1; Gaps 1;

QY 1 MNNVLANGRRTTCDAYNVVAHDPFSEHKSIDTIRKEMWEMKRTDHSIYVAVTVSSSF 60
 DB 1 MNNVLANGRRTTCDAYNVVAHDPFSEHKSIDTIRKEMWEMKRTDHSIYVAVTVSSSF 60

QY 61 LKKVGSILGKRIILSELNGLIFPSGSTNIMODILRETFQFNORLNTDTLAVNAELTGL 120
 DB 61 LKKVGSILGKRIILSELNGLIFPSGSTNIMODILRETFQFNORLNTDTLAVNAELTGL 120

QY 121 QANIRENOQVDFNLPONPVPVLSTSSVTNMOQLFNLRLPQFRVQGYQLLLPLPQA 180
 DB 121 QANIRENOQVDFNLPONPVPVLSTSSVTNMOQLFNLRLPQFRVQGYQLLLPLPQA 180

QY 181 ANHLSFIRDVLANDEWGISAAITLRTYONVKNITTEYSNVCINTYQAFEGANTLHD 240
 DB 181 ANHLSFIRDVLANDEWGISAAITLRTYONVKNITTEYSNVCINTYQAFEGANTLHD 240

QY 241 MLEPRTYMFANFEVYSIWSLFFKQSLVSSGANLYASGGPQOTQSFISQDMPPLYSLE 300
 DB 241 MLEPRTYMFANFEVYSIWSLFFKQSLVSSGANLYASGGPQOTQSFISQDMPPLYSLE 300

QY 301 QVNSNYVLNGFSGARLTQTPENIGLPPTTTTHALLAARVYSGVSGSDI-GAVFNQNF 359
 DB 301 QVNSNYVLNGFSGARLTQTPENIGLPPTTTTHALLAARVYSGVSGSDI-GAVFNQNF 359

QY 360 SCSTPLPPLTFPVYSMDSGSDRGVNTVMWQTESFESTLRCGATFARGSNVFPD 419
 DB 360 SCSTPLPPLTFPVYSMDSGSDRGVNTVMWQTESFESTLRCGATFARGSNVFPD 419

QY 420 NCNTISPLSTSFVMSWLDSDGQGVTTVMQTESFESTLRCGATFARGSNVFPD 420
 DB 420 NCNTISPLSTSFVMSWLDSDGQGVTTVMQTESFESTLRCGATFARGSNVFPD 420

QY 420 YFIRNISGVLVWNEEDLRRLPLHNEINISPSGCTGGLRAMYSVNRKNNTIYAHEN 479
 DB 421 YFIRNISGVLVWNEEDLRRLPLHNEINISPSGCTGGLRAMYSVNRKNNTIYAHEN 480

QY 480 GTMHLAPEDYGFETISPHATOVNNQRTFISEKFGQSDSLREPOSNTARATTLGNG 539
 DB 481 GTMHLAPEDYGFETISPHATOVNNQRTFISEKFGQSDSLREPOSNTARATTLGNG 540

QY 540 NSYNLYRYSLSIGNSTIRNTINGRYTASNNVTNNNDGYNNGARPLDIMGVAVASDN 599
 DB 541 NSTNLRYRYSLSIGNSTIRNTINGRYTASNNVTNNNDGYNNGARFSDINIGVAVASDN 600

QY 600 TNPVLDINVTNSGTQFELNINIFVPTNIPPIY 632
 DB 601 SDVPLDINVTNSGTQFELNINIFVPTNIPPIY 633

RESULT 8

US-09-041-991A-8
 Sequence 8, Application US/09041991A
 Patent No. 6107278

GENERAL INFORMATION:

APPLICANT: Schnepf, H. Ernest
 Narva, Kenneth E.
 Muller-Cohn, Judy

TITLE OF INVENTION: Toxins Active Against Peets

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
 STREET: 2421 N.W. 41st Street, Suite A-1
 CITY: Gainesville
 STATE: Florida
 COUNTRY: USA
 ZIP: 32606

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/041,991A
 FILING DATE: 13-MAR-1998

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
 NAME: Sanders, Jay M.
 REGISTRATION NUMBER: 39,355
 REFERENCE/DOCKET NUMBER: MA-709

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (352) 375-8100
 TELEFAX: (352) 372-5800

INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 633 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-041-991A-8

Query Match

Best Local Similarity 87.8%; Score 2913.5; DB 3; Length 633;
 Matches 552; Conservatve 42; Mismatches 38; Indels 1; Gaps 1;

QY 1 MNNVLANGRRTTCDAYNVVAHDPFSEHKSIDTIRKEMWEMKRTDHSIYVAVTVSSSF 60
 DB 1 MNNVLANGRRTTCDAYNVVAHDPFSEHKSIDTIRKEMWEMKRTDHSIYVAVTVSSSF 60

QY 61 LKKVGSILGKRIILSELNGLIFPSGSTNIMODILRETFQFNORLNTDTLAVNAELTGL 120
 DB 61 LKKVGSILGKRIILSELNGLIFPSGSTNIMODILRETFQFNORLNTDTLAVNAELTGL 120

QY 121 QANIRENOQVDFNLPONPVPVLSTSSVTNMOQLFNLRLPQFRVQGYQLLLPLPQA 180
 DB 121 QANIRENOQVDFNLPONPVPVLSTSSVTNMOQLFNLRLPQFRVQGYQLLLPLPQA 180

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121 QANVEERQVDNFIAPNKNVPLSTSSVNTMOQLFNRLSQOMOGYOLLPLPFOA 180
181 ANMLSPTRDVLINADWEGISAAITRTYQNTLKNVTEYSNCINTYQAFRGALTRHD 240
181 ANMLSPTRDVLINADWEGISAAITRTYQNTLKNVTEYSNCINTYQAFRGALTRHD 240
181 ANMLSPTRDVLINADWEGISAAITRTYQNTLKNVTEYSNCINTYQAFRGALTRHD 240
241 MEERTYMLNVEEYVSIWLSFKYQSLVSSGANLYASGSGPOQTOSFTSQDWPELYSLF 300
241 MEERTYMLNVEEYVSIWLSFKYQSLVSSGANLYASGSGPOQTOSFTSQDWPELYSLF 300
301 QVNSVYVINGSGSARLTOTFPNIGLPGTTTTALLAAVYVSGVSSGI -GAVFNQNF 359
301 QVNSVYVINGSGSARLTOTFPNIGLPGTTTTALLAAVYVSGVSSGI -GAVFNQNF 359
301 QVNSVYVINGSGSARLTOTFPNIGLPGTTTTALLAAVYVSGVSSGI -GAVFNQNF 359
360 SCSTFLPPLTTPFVRSWLDGSDRGVNTVNMQTESFESTLGLRCGAFARGNSNYFPD 419
361 NCNTISPLSTSPFRIWLDGSDRGVNTVNMQTESFESTLGLRCGAFARGNSNYFPG 420
420 YFIRNIGSVPLVARNEDLRPLHYNEIRNIESPSGTPGGLRAYVSVHNRKNNTYVAHEN 479
421 YFIRNIGSVPLVARNEDLRPLHYNEIRNIESPSGTPGGLRAYVSVHNRKNNTYVAHEN 480
480 GTHMLAPEDYGTFTISPIHATQVNNQTRTFISEKFGQSDSLRFGOSNTTAYTLRGNG 539
481 GTHMLAPEDYGTFTISPIHATQVNNQTRTFISEKFGQSDSLRFGOSNTTAYTLRGNG 540
540 NSYNLYRVSSLGNSITRTINGRYTASNTTNNNDGVNNGARFLDINKGNVYASDN 599
541 NSYNLYRVSSLGNSITRTINGRYTASNTTNNNDGVNNGARFLDINKGNVYASDN 600
600 TNPVPLDINTVNSGTQFELMIMVPTNLPPIY 632
601 SDVPLDINTVNSGTQFELMIMVPTNLPPIY 633

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RESULT 9
 US-09-608-533a-8
 Sequence 8, Application US/09608533A
 Patent No. 6534644
 GENERAL INFORMATION:
 APPLICANT: Schneck, H. Ernest
 Narva, Kenneth E.
 Muller-Cohn, Judy
 TITLE OF INVENTION: Toxins Active Against Pests
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESS: 2421 N.W. 41st Street, Suite A-1
 City: Gainesville
 STATE: Florida
 COUNTRY: USA
 ZIP: 32606
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/608,533A
 FILING DATE: 30-Jun-2000
 CLASSIFICATION: <Unknown>
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 09/041,991
 FILING DATE: 13-MARCH-1998
 ATTORNEY/AGENT INFORMATION:
 NAME: Sanders, Jay M.
 REGISTRATION NUMBER: 39 355
 REFERENCE/DOCKET NUMBER: MA-709D1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (352) 375-8100
 TELEFAX: (352) 372-5800
 INFORMATION FOR SEQ ID NO: 8:

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SEQUENCE CHARACTERISTICS:
LENGTH: 633 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-608-533a-8
Query Match      87.9%; Score 2913.5; DB 4; Length 633;
Best Local Similarity 87.2%; Pred. No. 5,3e-251;
Matches 552; Conservative 42; Mismatches 38; Indels 1; Gaps 1;

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RESULT 10
 US-09-041-991A-6
 Sequence 6, Application US/09041991A
 Patent No. 6107278
 GENERAL INFORMATION:
 APPLICANT: Schneck, H. Ernest
 Narva, Kenneth E.
 Muller-Cohn, Judy
 TITLE OF INVENTION: Toxins Active Against Pests
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESS: 2421 N.W. 41st Street, Suite A-1
 City: Gainesville
 STATE: Florida

```

COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,991A
FILING DATE: 13-MAR-1998
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-709
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 623 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-041-991A-6

Query Match
Best Local Similarity 78.8%; Score 2610.5; DB 3; Length 623;
Matches 508; Conservative 46; Mismatches 68; Indels 11; Gaps 6;

QY 1 MNNVLANGRTTICDAVNVVAHDPSPFEHKSJLDTIRKEMWKRTHSLYVAPIVGTVSF 60
DB 1 MNNVLANGRTTICDAVNVVAHDPSPFEHKSJLDTIRKEMWKRTHSLYVAPIVGTVSF 60
QY 61 LKRVGSLIKRILSLMGLIFPSGSTNLMODILRETEOPINORLNTTLARVAELRGL 120
DB 61 LKRVGSLIKRILSLMGLIFPSGSTNLMODILRETEOPINORLNTTLARVAELRGL 120
QY 121 QANIRENOVDNPLNPTQNPVPLSTSSVNTMOQLFLNLPQFRVGYQLLLPLFAQA 180
DB 121 QANIRENOVDNPLNPTQNPVPLSTSSVNTMOQLFLNLPQFRVGYQLLLPLFAQA 180
QY 121 QANVAFNRQVDNPLNPNQNPVPLAIDSVTLOQLFLSLRPLQFQIGYQLLLPLFAQA 180
DB 121 QANVAFNRQVDNPLNPNQNPVPLAIDSVTLOQLFLSLRPLQFQIGYQLLLPLFAQA 180
QY 181 ANNELSFIRVDVNLNADDEMGISAATLRTYONYLKNYTTESYNCINTYOTAFRGINTRLHD 240
DB 181 ANNELSFIRVDVNLNADDEMGISAATLRTYONYLKNYTTESYNCINTYOTAFRGINTRLHD 240
QY 181 ANHLSPTRVDVNLNADDEMGISAATVRYTRDHLRFTRDYSNVCINTYOTAFRGINTRLHD 240
DB 181 ANHLSPTRVDVNLNADDEMGISAATVRYTRDHLRFTRDYSNVCINTYOTAFRGINTRLHD 240
QY 241 MLEFRTYMLNVEFYVSIWLSLFXQSILVSSGANLYASGSGP--TOSPTAHNMPFLYSLF 300
DB 241 MLEFRTYMLNVEFYVSIWLSLFXQSILVSSGANLYASGSGP--TOSPTAHNMPFLYSLF 300
QY 301 QVNSVYVINGSGARLTQTFPNIGLPGTTTTHALLAARVNSGVSAGDIG-AVENQNF 359
DB 301 QVNSVYVINGSGARLTQTFPNIGLPGTTTTHALLAARVNSGVSAGDIG-AVENQNF 359
QY 299 QVNSVYVINGSGARLTQTFPNIGLPGTTTTHALLAARVNSGVSAGDIG-AVENQNF 358
DB 299 QVNSVYVINGSGARLTQTFPNIGLPGTTTTHALLAARVNSGVSAGDIG-AVENQNF 358
QY 360 SCSTFLPPLLPFRWSLDSGRGVNTVNMOTBSFSTGLRGCATFARKNSVYFPD 419
DB 360 SCSTFLPPLLPFRWSLDSGRGVNTVNMOTBSFSTGLRGCATFARKNSVYFPD 419
QY 359 NISTLPNLOPFRKSWLDSGRGVNTVNMOTBSFSTGLRGCATFARKNSVYFPD 417
DB 359 NISTLPNLOPFRKSWLDSGRGVNTVNMOTBSFSTGLRGCATFARKNSVYFPD 417
QY 420 YFIRNISGVPLVWNEEDLRPLAHYNEIRNIESPSTPGGLRAYMVSVNKRNIYAVHN 479
DB 420 YFIRNISGVPLVWNEEDLRPLAHYNEIRNIESPSTPGGLRAYMVSVNKRNIYAVHN 479
QY 418 YFIRNISGVPLVWNEEDLRPLAHYNEIRNIESPSTPGGLRAYMVSVNKRNIYAVHN 471
DB 418 YFIRNISGVPLVWNEEDLRPLAHYNEIRNIESPSTPGGLRAYMVSVNKRNIYAVHN 471
QY 480 GTHMLAPEDYTGFTSLPIHATOVNNOQRTISKNGOGDRLREOSNTTAYTRKNG 539
DB 480 GTHMLAPEDYTGFTSLPIHATOVNNOQRTISKNGOGDRLREOSNTTAYTRKNG 539
QY 472 GTHMLAPEDYTGFTSLPIHATOVNNOQRTISKNGOGDRLREOSNTTAYTRKNG 531
DB 472 GTHMLAPEDYTGFTSLPIHATOVNNOQRTISKNGOGDRLREOSNTTAYTRKNG 531
QY 540 NSYNTLYRVSGLNSTIRVINGRYTASVNTTNDGVNNGARFELDINMGVVASDN 599
DB 540 NSYNTLYRVSGLNSTIRVINGRYTASVNTTNDGVNNGARFELDINMGVVASDN 599
QY 532 NSYNTLYRVSGLNSTIRVINGRYTASVNTTNDGVNNGARFELDINMGVVASDN 590
DB 532 NSYNTLYRVSGLNSTIRVINGRYTASVNTTNDGVNNGARFELDINMGVVASDN 590
QY 600 TNPPLDINVTENSGTOPELNMIMFPTNLPPIY 632
DB 600 TNPPLDINVTENSGTOPELNMIMFPTNLPPIY 632

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DB 591 TNPPLDINVTENSGTOPELNMIMFPTNLPPIY 623

RESULT 11
US-09-608-533A-6
Sequence 6, Application US/09608533A
Patent No. 6534644
GENERAL INFORMATION:
APPLICANT: Schnepf, H. Ernest
Narva, Kenneth E.
Miller, Cohn, Judy
TITLE OF INVENTION: Toxins Active Against Pests
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/608,533A
FILING DATE: 30-Jun-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/041,991
FILING DATE: 13-MARCH-1998
ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-709D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 623 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-608-533A-6

Query Match
Best Local Similarity 78.8%; Score 2610.5; DB 4; Length 623;
Matches 508; Conservative 46; Mismatches 68; Indels 11; Gaps 6;

QY 1 MNNVLANGRTTICDAVNVVAHDPSPFEHKSJLDTIRKEMWKRTHSLYVAPIVGTVSF 60
DB 1 MNNVLANGRTTICDAVNVVAHDPSPFEHKSJLDTIRKEMWKRTHSLYVAPIVGTVSF 60
QY 61 LKRVGSLIKRILSLMGLIFPSGSTNLMODILRETEOPINORLNTTLARVAELRGL 120
DB 61 LKRVGSLIKRILSLMGLIFPSGSTNLMODILRETEOPINORLNTTLARVAELRGL 120
QY 121 QANIRENOVDNPLNPTQNPVPLSTSSVNTMOQLFLNLPQFRVGYQLLLPLFAQA 180
DB 121 QANIRENOVDNPLNPTQNPVPLSTSSVNTMOQLFLNLPQFRVGYQLLLPLFAQA 180
QY 121 QANVAFNRQVDNPLNPNQNPVPLAIDSVTLOQLFLSLRPLQFQIGYQLLLPLFAQA 180
DB 121 QANVAFNRQVDNPLNPNQNPVPLAIDSVTLOQLFLSLRPLQFQIGYQLLLPLFAQA 180
QY 181 ANNELSFIRVDVNLNADDEMGISAATLRTYONYLKNYTTESYNCINTYOTAFRGINTRLHD 240
DB 181 ANNELSFIRVDVNLNADDEMGISAATLRTYONYLKNYTTESYNCINTYOTAFRGINTRLHD 240
QY 181 ANHLSPTRVDVNLNADDEMGISAATVRYTRDHLRFTRDYSNVCINTYOTAFRGINTRLHD 240
DB 181 ANHLSPTRVDVNLNADDEMGISAATVRYTRDHLRFTRDYSNVCINTYOTAFRGINTRLHD 240
QY 241 MLEFRTYMLNVEFYVSIWLSLFXQSILVSSGANLYASGSGP--TOSPTAHNMPFLYSLF 300
DB 241 MLEFRTYMLNVEFYVSIWLSLFXQSILVSSGANLYASGSGP--TOSPTAHNMPFLYSLF 300
QY 301 QVNSVYVINGSGARLTQTFPNIGLPGTTTTHALLAARVNSGVSAGDIG-AVENQNF 359
DB 301 QVNSVYVINGSGARLTQTFPNIGLPGTTTTHALLAARVNSGVSAGDIG-AVENQNF 359
QY 299 QVNSVYVINGSGARLTQTFPNIGLPGTTTTHALLAARVNSGVSAGDIG-AVENQNF 358
DB 299 QVNSVYVINGSGARLTQTFPNIGLPGTTTTHALLAARVNSGVSAGDIG-AVENQNF 358
QY 360 SCSTFLPPLLPFRWSLDSGRGVNTVNMOTBSFSTGLRGCATFARKNSVYFPD 419
DB 360 SCSTFLPPLLPFRWSLDSGRGVNTVNMOTBSFSTGLRGCATFARKNSVYFPD 419
QY 359 NISTLPNLOPFRKSWLDSGRGVNTVNMOTBSFSTGLRGCATFARKNSVYFPD 417
DB 359 NISTLPNLOPFRKSWLDSGRGVNTVNMOTBSFSTGLRGCATFARKNSVYFPD 417
QY 420 YFIRNISGVPLVWNEEDLRPLAHYNEIRNIESPSTPGGLRAYMVSVNKRNIYAVHN 479
DB 420 YFIRNISGVPLVWNEEDLRPLAHYNEIRNIESPSTPGGLRAYMVSVNKRNIYAVHN 479
QY 418 YFIRNISGVPLVWNEEDLRPLAHYNEIRNIESPSTPGGLRAYMVSVNKRNIYAVHN 471
DB 418 YFIRNISGVPLVWNEEDLRPLAHYNEIRNIESPSTPGGLRAYMVSVNKRNIYAVHN 471
QY 480 GTHMLAPEDYTGFTSLPIHATOVNNOQRTISKNGOGDRLREOSNTTAYTRKNG 539
DB 480 GTHMLAPEDYTGFTSLPIHATOVNNOQRTISKNGOGDRLREOSNTTAYTRKNG 539
QY 472 GTHMLAPEDYTGFTSLPIHATOVNNOQRTISKNGOGDRLREOSNTTAYTRKNG 531
DB 472 GTHMLAPEDYTGFTSLPIHATOVNNOQRTISKNGOGDRLREOSNTTAYTRKNG 531
QY 540 NSYNTLYRVSGLNSTIRVINGRYTASVNTTNDGVNNGARFELDINMGVVASDN 599
DB 540 NSYNTLYRVSGLNSTIRVINGRYTASVNTTNDGVNNGARFELDINMGVVASDN 599
QY 532 NSYNTLYRVSGLNSTIRVINGRYTASVNTTNDGVNNGARFELDINMGVVASDN 590
DB 532 NSYNTLYRVSGLNSTIRVINGRYTASVNTTNDGVNNGARFELDINMGVVASDN 590
QY 600 TNPPLDINVTENSGTOPELNMIMFPTNLPPIY 632
DB 600 TNPPLDINVTENSGTOPELNMIMFPTNLPPIY 632

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QY 301 QVNSNYVLNGFSGARLLTOTFPNIGLPGTTTTALLARUNYSGVSGDGL-AVENONF 359
 DB 299 QVNSNYVLNGFSGARLLTOTFPNIGLPGTTTTALLARUNYSGVSGDGL-AVENONF 358
 QY 360 SCSTFLPPLTFFVSMWLDSCDRGVNTVMQTESFEFTGLRGCAFTARGNSNYPD 419
 DB 359 NISTLFPNIGTPIRSMWLDSCDRGVNTVMQTESFEFTGLRGCAFTARGNSNYPD 417
 QY 420 YFNIISGVPLVVRNEDLRRLAHNEIRNIESPESGPGGLAVVSNHRKNNIYAHEH 479
 DB 418 YFNIISGVPLVVRNEDLRRLAHNEIRNIESPESGPGGLAVVSNHRKNNIYAHEH 471
 QY 480 GTMHLAPEDYGTFTSPHATOVNNQTRTFISEKFGQDGLRFEQSNITARYTLRNG 539
 DB 472 GTMHLAPEDYGTFTSPHATOVNNQTRTFISEKFGQDGLRFEQSNITARYTLRNG 531
 QY 540 NSYULYRVSLSGNTIRVTINGRVTASVNTTNNQVNDGAPFLDINMGVVASDN 599
 DB 532 NSYULYRVSLSGNTIRVTINGRVTASVNTTNNQVNDGAPFLDINMGVVASDN 590
 QY 600 TIVPDLINVTENSGTQFELANIMEFVPTNLEPIY 632
 DB 591 TIVPDLINVTENSGTQFELANIMEFVPTNLEPIY 623

RESULT 12
 US-09-408-820-2
 ; Sequence 2, Application US/0940820
 ; Patent No. 6204057
 ; GENERAL INFORMATION:
 ; APPLICANT: Schmeiter, Wolfgang
 ; APPLICANT: Krieger, Lutz
 ; TITLE OF INVENTION: Polynucleotides And The Proteins Encoded Thereby,
 ; FILE REFERENCE: S-30403/A/OHD/GG1986/PCT
 ; CURRENT APPLICATION NUMBER: US/09/408,820
 ; EARLIER FILING DATE: 1999-09-29
 ; EARLIER APPLICATION NUMBER: 09/051,454
 ; EARLIER FILING DATE: 1998-04-07
 ; EARLIER APPLICATION NUMBER: DE 195 40 223.5
 ; NUMBER OF SEQ ID NOS: 2
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 706
 ; TYPE: PRT
 ; ORGANISM: Bacillus popilliae
 ; FEATURE:
 ; OTHER INFORMATION: strain subspecies: melolonthae H1; stage of
 ; OTHER INFORMATION: development: spore stage; cell type: sporangium
 ; FEATURE:
 ; OTHER INFORMATION: immediate origin: isolate from the haemolymph of
 ; OTHER INFORMATION: Melolontha melolontha individuals captured on open
 ; OTHER INFORMATION: ground
 ; NAME/KEY: PEPTIDE
 ; LOCATION: (1)..(706)
 ; OTHER INFORMATION: mature protein crystal peptide determined by
 ; OTHER INFORMATION: experiment
 ; US-09-408-820-2

Query Match 32.6%; Score 1080; DB 3; Length 706;
 Best Local Similarity 38.4%; Pred. No. 1,7e-87;
 Matches 264; Conservative 96; Mismatches 233; Indels 94; Gaps 21;

QY 2 NVVANN-----GRITICDA-----YVVADPPSPFKSLDTIRKEMWKRTD 45
 DB 58 NNDNNDAICBGLGTIDNNITCSTDFPINVRDP--FKKSTQGLIRKEMWKRTD 115
 QY 46 HSLVYAPVIGTVSSFLIKKVGSLIGKRLISEKGLIPSGSTNNMODLAKETQFQNL 105
 DB 116 PSIFTPAIVGVVTSFLQSLIKQKQATSLFKTLTDLLFPNNSSLTMEILRATBOYOERTL 175

QY 106 NDTLAPVNAELFGLQANIREFNOQVDFNPTONVPLSITSVNTMOQLFLNRLPQR 165
 DB 176 DDTLAPVNAELFGLQANIREFNOQVDFNPTONVPLSITSVNTMOQLFLNRLPQR 235
 QY 166 VQGYQVLLPLFPAQANMLSTRVULNADENGICSAATLRYQNYLKNNTSYNYCN 225
 DB 236 VQGYQVLLPLFPAQANMLSTRVULNADENGICSAATLRYQNYLKNNTSYNYCN 295
 QY 226 TYQAFRGANTR-----LHMLERFTYMFANVEYSIWSLFEKYSILVSSGANDYASG 279
 DB 296 TYQAFRGANTR-----LHMLERFTYMFANVEYSIWSLFEKYSILVSSGANDYASG 352
 QY 280 SGPQOTQSTQDMPLYSIFQVNSNYVLNGFSGARLLTOTFPNIG-----LPGTTTH 333
 DB 353 DNKMEGAVPISYGPFPNSYIOTKSNVYLSGVSGIGARFTYSTVIGKYLHDLKNITTT 411
 QY 334 ALTAARVYSGVSSGDIGAVN-----QNFSCSTFLP-PLLTTP 371
 DB 412 -----YGGGTGQPMIGVQLSTTELDLKKQQAATRDGLVDFOFPLNCLM.PNPTTAP 463
 QY 372 -FVSMWLDG--SDRGVNTVMQTESFEFTGL-RGCAFTARGNSNYPDFIRNIGV 428
 DB 464 YFATSLYBSRYSISGVLKRDVFKSE--DSTGAGNPAWTS-----YDYITNHSAT 515
 QY 429 PLVVRNEDLRRLAHNEIRNIESPESGPGGLAVVSNHRKNNIYAHEHGMHLADE 488
 DB 516 VQINGENDTTPPLVYFENREPTSTRGV-----NKVIYVNRKANIAGTNGMTIHQADP 570
 QY 489 DYGTFTSPHATOVNNQTRTFISEKFGQDGLRFEQSNITARYTLRNG-NSYULYR 547
 DB 571 DGTGFTVSPHESA--WTITSYKENGSGDGLH--KGGLIHLMLSGNQDPRYLVAR 627
 QY 548 VSSLSGNTIRVTINGRVTASVNTTNNQVNDGAPFLDINMGV-VASDNTVPLD 605
 DB 628 LSGAN---QVLSQPTTSIYAFDSTINNEGIDTNGSKFDFAFSTPVIBEOK-----E 679
 QY 606 INTFENSGTQFELANIMEFVPTNLEPIY 632
 DB 680 IVTFEGVSLDMLNLIPLPADUTPLV 706

RESULT 13
 US-08-793-331-7
 ; Sequence 7, Application US/0879331
 ; Patent No. 6071877
 ; GENERAL INFORMATION:
 ; APPLICANT: DELECLUSE, ARMELE
 ; APPLICANT: THIERY, ISABELLE
 ; TITLE OF INVENTION: NEW POLYPEPTIDES HAVING A TOXIC ACTIVITY AGAINST
 ; FILE REFERENCE: 0660-0116-0 PCT
 ; CURRENT APPLICATION NUMBER: US/08/793,331
 ; EARLIER FILING DATE: 1997-05-13
 ; EARLIER APPLICATION NUMBER: PCT/FR95/01116
 ; EARLIER FILING DATE: 1995-08-24
 ; EARLIER APPLICATION NUMBER: FR 94/10299
 ; EARLIER FILING DATE: 1994-08-25
 ; NUMBER OF SEQ ID NOS: 15
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 7
 ; LENGTH: 644
 ; TYPE: PRT
 ; ORGANISM: B. thuringiensis ser. israelensis
 ; US-08-793-331-7

Query Match 10.2%; Score 336.5; DB 3; Length 644;
 Best Local Similarity 23.1%; Pred. No. 2.7e-21;
 Matches 167; Conservative 98; Mismatches 257; Indels 201; Gaps 34;

QY 27 EHKSLDTIRKEMWKRTDHSLY-----VAP---YGVVSSFLIKKVGSLIGKRLISE 76
 DB 3 EDSLSLTLISV-----NETDFPINNTTEPTIRPALINAVPAIQAQYLTATGKAKAAAFSK 58

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QY 77 LMGLEPSSGNTLMODILRETEOFLNORLNTTLARVNALEGLQANIREFNOQVNL- 135
DB 59 VLSLIFPGSQPATMEKVAETEVELLINQKLSQBRVILNABRG-----LLEVSDFVAYIK 114
QY 136 NPTQNVPLSTISSVNMQOELN-----RLPQFVQOYQLLLPLPQAAMHLSP 188
DB 115 QPQFTPA-----TAKGYFLNLSGAILIQLPQFEVQYBEVSIALFTQWCTLHLTL 165
QY 189 RDVLNADWEGISAATLRTYQNYLKNYTERSVNCTNYQTA-RCGLNTRLHDLERFY 247
DB 166 KQGLILAGSAMGFTQADVDFIKLQKQVADRTMLMAMYTEERGLCKVSLKQGLTRK 225
QY 248 MFLNVEYVSIWLSFKYOSLLVSSGANLYASSGPQOTQSFYSQWPLYSLFQVNSN- 305
DB 226 CNLYPPPAKMSLMKREGLKQSSLSL-----WDYGVGISIPVANNM 268
QY 306 ----YVINGSGARLTQTEPNIGLPGTTTHALLAARVNSG-----GVSSGDIQAVF 355
DB 269 GGLVYKLMGVEVNOQLTVKFN-----SFTNEPADIPARENIRGVHPIYDSSGLTWIG 324
QY 356 N---QWFGSGTFPLPLTPPVRSMLDSDGQVNTYTNQ----- 393
DB 325 NGRTNENPAD-----NNGEIMEVRIQTQYQNPNEPIAPEDIIINOILTA 370
QY 394 -----TESFESTL---GLRCGAFIARGN-----SNY--FPDYFIANI 425
DB 371 PAPADLFFKNADINWKFQFOSLYGNWIKLGTQVLSRGITLPRVYLAYQGYIRAI 430
QY 426 SGVPLVVR---NEDLRPHVNEINISPSG-----TPGLAAVNSVHNRKNITYA 475
DB 431 SACPRGVLAINHL--TLLTYNRI--EYDPTTENIIVGAPRNTKDF-----YSKKS--- 480
QY 476 VHENGTMLHAPEDYGTFTISPIHATOVNNTQTFISEKFGNQGD-SLREOG--NTAR 532
DB 481 ----HYLSTNDSYVIALQPAEVS---SSFLDPTDQATGSIKFAFFISNEAK 530
QY 533 YTLRGNSVNYLYRVSISLGNSTIIVTINGVYTAENVNTTNDGVNDGAFILINNG 592
DB 531 YSIRLNL-TGFVITATRYKLT---LKVRYVYTL--PAGIVGQNSGNN---RMLGSFTA 579
QY 593 NV-----VASDNTVPLDINV--TPNSGTQFELIMIMFV-----PTNL 628
DB 580 NNPBWWDFTYDAFTNDLIGITTSSTNALFSISSDSINSIGERWYQLFLVKSAPFTQI 639
QY 629 PPI 631
DB 640 NPL 642

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RESULT 14
US-08-286-870A-4
Sequence 4, Application US/08286870A
Patent No. 6063605
GENERAL INFORMATION:
APPLICANT: ELY, S
APPLICANT: TAILOR, RH
APPLICANT: TIPPETT, JM
APPLICANT: BLENK, RG
TITLE OF INVENTION: BACTERIAL GENES
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DABRY & CUSHMAN
ADDRESSEE: Intellectual Property Group of
PILLSBURY, MADISON & SUTRO LLP
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286, 870A
FILING DATE: 05-AUG-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/520228
FILING DATE: 09-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 8910624.9
FILING DATE: 09-MAY-1989
ATTORNEY/AGENT INFORMATION:
NAME: PAUL N. KOKULIS
REGISTRATION NUMBER: 16, 773
REFERENCE/DOCKET NUMBER: 70608/220720
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 648 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-286-870A-4

Query Match      9.9%; Score 327.5; DB 3; Length 648;
Best Local Similarity 22.8%; Pred. No. 1.7e-20;
Matches 162; Conservative 103; Mismatches 271; Indels 173; Gaps 32;

QY 21 HDPSFEHK-----SLDTRKEM-MEMKRTDH-----SLY--VAP----- 52
DB 9 HQSSSNAXKXDKSIDSLAKMETDELQINNHEDCLAKSEYNEFPVSAITQIGIAG 68
QY 53 -IVTVSSFLKKVQSLGKRIISELMGLIFSSGNTLMODILRETEOFLNORLNTDTLA 111
DB 69 KILDTLVPPAQVAVSLY-SFLIGELM---FKGR-NQWEIFMEHVEEIIINOKISTYARN 122
QY 112 RVNAELSGLOANIREFNOQVNFPLNPTQNPVLSIT-SSVNTMOQLFLNRLPQFVQOY 170
DB 123 KALTDLKGIGDALVAYHDSLESWGNRRNTRARSVYSQYIAELMFYQKLSFVSGEE 182
QY 171 LLLLEPLQAAMHLSFRDVLNADWEGISAATLRTYQNYLKNYTERSVNCTNYQTA 230
DB 183 VLLPLIYQAANLHLLLLRDASIFGKRWGLSSSEISTFYNRQVERAGDYSDHCWYSTG 242
QY 231 FRGL-NTRLHDLML---EFRTYMEFLNVEYVSIWLSFKYOSILVSSGANL---YASGSGP 282
DB 243 LNNLRGTNAESWVRVYQFRDMTLMVLDLVALFPSYDTQWYPIKTRQULREYVITDAIGT 302
QY 283 QQTO-SFTSODW-----PFL-----YSLFQVNSN-YVINGPSG 313
DB 303 VHPHPSFTITWYNNNAEFSALAAVNPPLDLFEOVTIYSLLSRWSTVOYNNMVG 362
QY 314 ARLTQTFPNIGLPGTTTHALLAARVNSGVSSGDIQAVFQNSGTFPLPLTPPV 373
DB 363 HKL--EFRTIGTINISF-----QSTNITSINVTLPFT 394
QY 374 RSWLDGSDRGQVNTV-----NMQ--TESFESTLGLRCGAFIARGNSTNFPD 419
DB 395 SRDVTESLADLNLPLTPQVNPVPRVDFHMKFVTHPIA-----DNFYPP 441
QY 420 YFRNISGVPLVVRNEDLRPHVNEINISPSGTGGLRAVNSVHNRKNITYA-VHE 478
DB 442 Y-----AGIGLOQDSNELPPEATQDPNYESYSHRLSHIG--LISASHV-KALVYSWTHR 494
QY 479 NGTMHAPEDYGTFTISPIHATOV-----NNGTRFISEKFG--NOGDSLAREGQNTTA 531
DB 495 SA-----DRTN-TIEPNSITQIPLKAPNLSGAAGVRRGPGTGADILR-KTNVTGT 543
QY 532 RYLRNGN-----SYLYIRVSSISLGNSTIIVTINGVYTAENVNTTNDGVNDGAF 586

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Fri Aug 15 11:51:34 2003

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Page 10

Db 544 FEDIRVNINPEFAORVIRIRVASTTDLQFTSINGKAINQNSFATNMR-----GSD 596
QY 587 LDINNGNVASDNTNVPDLINVT-----FNSGTQFELMNTMFPVPTL 628
Db 597 LDYKFRVTVGFTTPEFSLDVOSTFTTGAMNFSGNEVYIDRIEFVPEV 645

RESULT 15
US-08-286-870A-8
Sequence 8, Application US/08286870A
Patent No. 6063605
GENERAL INFORMATION:
APPLICANT: ELY, S
APPLICANT: TAYLOR, RH
APPLICANT: TIPPETT, JM
APPLICANT: BLENK, RG
TITLE OF INVENTION: BACTERIAL GENES
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESSES:
ADDRESSEE: CUSHMAN DABRY & CUSHMAN
ADDRESSEE: Intellectual Property Group of
ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,870A
FILING DATE: 05-AUG-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/520228
FILING DATE: 09-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 8910624.9
FILING DATE: 09-MAY-1989
ATTORNEY/AGENT INFORMATION:
NAME: PAUL N. KOKULIS
REGISTRATION NUMBER: 16, 773
REFERENCE/DOCKET NUMBER: 70608/220720
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 719 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-286-870A-8

Query Match 9.9%; Score 327.5; DB 3; Length 719;
Best Local Similarity 22.8%; Pred. No. 2e-20;
Matches 162; Conservative 103; Mismatches 271; Indels 173; Gaps 32;

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Db 9 HOSFSSNAKVDKISTSLKNETDIDLOININHEDCLMSEYENVEPVASASTIQIGIAG 68
QY 53 -IVGVSSFLKKVGLIGRIILISELMLIFPSGSNTLMQDILRETPQFLNRLNTDTLA 111
Db 69 KILGTLGVPRAGVASY-SFLIGELW-----PKGK-NQWEIMEHVEEIIINQKISTYARN 122
QY 112 RVNALEBGLQNTREKQVDNPLAPNPVPLSIT-SSVNTMOQLFLNRLPQRFVQGYO 170
Db 123 KALTLKGLGDLALAVYHDSLESWGNRRNTRARSVVSQYIALELMFVOKLPSFAVSSEE 182

QY 171 LLLPLPFAAMNHSPFIRDVVLNADBEKISATLRTYQNTLKNVTTETYSNCTNFTYQTA 230
Db 183 VPLPIYAOANLHLLLRDASIGKEMGSSSEISTYNNQVERAGDSDHCVMKSTG 242
QY 231 FRGL-NTRLHML--ERRTYMFLANVEYVSIWSLFXKQSLVSSGANN-----VASGSGP 282
Db 243 LNNLRGTNASWVRXNQFRDMTLMVLADLALPESYIDQMPIKTNQLTREYVDAIGT 302
QY 283 QOTQ-SFTSODM-----PFL-----YSLFQVNSN-YVLNGPSG 313
Db 303 VHPHSFSTSTWYNNNAPSFAIBAAVRNPHLDLFELQVYVYSLSRWSNQYNNMMWG 362
QY 314 ARTVOTEPNIGLPGITTHALLAARVNVSGVSGDGAIVENONFSCSTPLPLTPFV 373
Db 363 HRL--EFTIGTGLNIST-----QSTNTSINPVTLPFT 394
QY 374 RSMIDSGSDRGVNTVT-----NMQ--TESPESITLRCGAFYAKGNSNYEPD 419
Db 395 SRDVYRTESLAGLNLPLQPVNGVPRVDPFMKKVTHPIAS-----DNFYPFG 441
QY 420 YFIRISGVPLVVRNEDLRPLHNEIRNIESPSGPGGLRAYVSVHNRKNNIYA-VHE 478
Db 442 Y----AGIGTQODENEELPPEATGQPNYESYSHLSHG--LISASHVKALVYSWTHR 494
QY 479 NGTMITHLAPEDYTGFTISPIHATQV-----NQRTFISEKFG-NQGBSLREQSNNTA 531
Db 495 SA-----DRTN-TIEPNSITQIPVKAFLNLSGAAVVGPGFTGQDILR-KTNIGT 543
QY 532 RYTLRNGN-----SYNLVAVSLSGNSITRTVINGRVYVTSNVTTNNNDGVNDGARF 586
Db 544 FEDIRVNINPEFAORVIRIRVASTTDLQFTSINGKAINQNSFATNMR-----GSD 596
QY 587 LDINNGNVASDNTNVPDLINVT-----FNSGTQFELMNTMFPVPTL 628
Db 597 LDYKFRVTVGFTTPEFSLDVOSTFTTGAMNFSGNEVYIDRIEFVPEV 645

Search completed: August 14, 2003, 18:13:21
Job time : 32 secs

Fri Aug 15 11:51:35 2003

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Page 1

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OM protein - protein search, using sw model

Run on: August 14, 2003, 18:11:07 ; Search time 28 Seconds
(without alignments)
2956,931 Million cell updates/sec

Title: US-10-040-906A-2

Sequence: 1 MNVIVNNGRTTICDANVVA.....GTQELMNTMPTVTLPTPY 632

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 492763 seqs, 131003257 residues

Total number of hits satisfying chosen parameters: 492763

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Published Applications AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/FCI_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
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7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
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14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	311.5	9.4	1156	US-10-099-285-72	Sequence 72, Appl
2	305.5	9.2	643	US-09-826-660-25	Sequence 25, Appl
3	305.5	9.2	1186	US-09-826-660-23	Sequence 23, Appl
4	275.5	8.3	1207	US-09-988-462-7	Sequence 7, Appl
5	272	8.2	1177	US-10-035-060-6	Sequence 6, Appl
6	269.5	8.1	667	US-10-032-717-8	Sequence 8, Appl
7	269.5	8.1	673	US-10-032-717-18	Sequence 18, Appl
8	269.5	8.1	1210	US-10-032-717-14	Sequence 4, Appl
9	268	8.1	1155	US-09-756-643-2	Sequence 9, Appl
10	268	8.1	1155	US-09-988-462-9	Sequence 9, Appl
11	268	8.1	1181	US-09-988-462-11	Sequence 11, Appl
12	268	8.1	1181	US-09-988-462-13	Sequence 13, Appl
13	268	8.1	1181	US-09-988-462-15	Sequence 15, Appl
14	268	8.1	1181	US-09-988-462-17	Sequence 17, Appl
15	268	8.1	1181	US-09-988-462-28	Sequence 28, Appl

16	267.5	8.1	1178	9	US-09-851-194-2	Sequence 2, Appl
17	266	8.0	1177	15	US-10-035-060-2	Sequence 2, Appl
18	265	8.0	605	9	US-09-826-660-4	Sequence 4, Appl
19	265	8.0	1148	9	US-09-826-660-2	Sequence 2, Appl
20	265	8.0	1174	9	US-09-826-660-6	Sequence 6, Appl
21	265	8.0	1177	9	US-09-873-873-34	Sequence 34, Appl
22	264	8.0	1177	15	US-10-035-060-8	Sequence 8, Appl
23	264	8.0	1179	15	US-10-035-060-8	Sequence 8, Appl
24	263	7.9	617	14	US-10-032-717-34	Sequence 34, Appl
25	263	7.9	670	14	US-10-032-717-24	Sequence 24, Appl
26	262.5	7.9	1177	9	US-09-873-873-28	Sequence 28, Appl
27	262.5	7.9	1177	11	US-09-997-914-28	Sequence 28, Appl
28	262	7.9	617	14	US-10-032-717-46	Sequence 46, Appl
29	262	7.9	670	14	US-10-032-717-44	Sequence 44, Appl
30	261.5	7.9	620	14	US-10-032-717-32	Sequence 32, Appl
31	261.5	7.9	673	14	US-10-032-717-22	Sequence 22, Appl
32	261.5	7.9	1156	9	US-09-826-660-15	Sequence 15, Appl
33	261.5	7.9	1177	9	US-09-873-873-26	Sequence 26, Appl
34	261.5	7.9	1177	11	US-09-997-914-26	Sequence 26, Appl
35	260.5	7.9	620	14	US-10-032-717-42	Sequence 42, Appl
36	260.5	7.9	673	14	US-10-032-717-40	Sequence 40, Appl
37	260.5	7.9	1163	9	US-09-756-526A-2	Sequence 2, Appl
38	260.5	7.9	1163	12	US-10-345-020-2	Sequence 2, Appl
39	260.5	7.9	1177	9	US-09-873-873-10	Sequence 10, Appl
40	260.5	7.9	1177	9	US-09-873-873-12	Sequence 12, Appl
41	260.5	7.9	1177	9	US-09-873-873-14	Sequence 14, Appl
42	260.5	7.9	1177	11	US-09-997-914-10	Sequence 10, Appl
43	260.5	7.9	1177	11	US-09-997-914-12	Sequence 12, Appl
44	260.5	7.9	1177	11	US-09-997-914-14	Sequence 14, Appl
45	258.5	7.8	616	14	US-10-032-717-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1
US-10-099-285-72
; Sequence 72, Application US/10099285
; Publication No. US20030105319A1

GENERAL INFORMATION:

APPLICANT: Schmeffel, H. Ernest
Wicker, Carol

Marva, Kenneth E.
Walz, Michelle

Stochoff, Brian
Muller-Cohn, Judy

TITLE OF INVENTION: Toxins Active Against Pests
NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanichik, Lloyd & Saliwanichik

STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville

STATE: Florida
COUNTRY: USA

ZIP: 32606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/099,285
FILING DATE: 15-Mar-2002

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/002,285
FILING DATE: <Unknown>

APPLICATION NUMBER: US 08/866,615
FILING DATE: 1-Jul-1997

APPLICATION NUMBER: US 08/674,002
FILING DATE: 1-Jul-1996

ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay M.

REGISTRATION NUMBER: 39,355
 REFERENCE/DOCKET NUMBER: MA-701C2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (352) 375-8100
 TELEFAX: (352) 372-5800
 INFORMATION FOR SEQ ID NO: 72:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1156 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 72:
 US-10-099-285-72

Query Match 9.4%; Score 311.5; DB 15; Length 1156;
 Best Local Similarity 23.3%; Pred. No. 3.5e-19;
 Matches 157; Conservative 96; Mismatches 221; Indels 199; Gaps 32;

QY 52 PIVGTSSFLKKVSGSLGKRLSELWGLIPSGSTNLMODILRETEQFLNQRLNTDTLA 111
 DB 87 PFGQIVSFY-----QFLNLTW-----PNDTALWEAKMQLVEELNQITEFARN 133
 QY 112 RNVALEGLQANIREFNOQVDFNLTNPONVPLSTTSVNTMOQLFLNRLPQFVQ 167
 DB 134 QALARLOGLDSFNVQKSLQWMLADNDTRNLSVYRAQFIADLDVNAIFLFAVN 190
 QY 168 GYQLILPLPAQANMLSFIDVVLNADWGISATLTQNTLYKNTTYSNCTINTY 227
 DB 191 GQVPLLSVYAAQVNHLLKDLASLGEEMGTQGEISTYDQLELTKNTNCEWY 250
 QY 228 QTA---PFGANT---RLHMLFEFTYMFANVEYISWISFKYQSLVSSGANLYASGS 280
 DB 251 NIGDLRLRGNTESMRYH---QFRREMLTVLVDV---ALFPYDV---RLYPTGS 298
 QY 281 GQOQTQS-FTS-----QDM-----PLY-----S 298
 DB 299 NQTLREYVYDPIFVPPANVGLCRWGTNPNTFSELENAPRPHLPRLNLSLTSSN 358
 QY 299 LFOVNSNYLVNGFSGARLTQTFPNIGLPG-----TTTTALLAARVNSGGVSSGDIG- 352
 DB 359 REPVSNNF-MDYNSGHTLRSLYNDASVQEDSYGLTTTTRATINPGVDGTRLESTAVDF 417
 QY 353 ---AVNQNFCSTFLPLLTTPVNSMLDSSD---RGVNTV---TMQTESPESLIG 402
 DB 418 RSALIGIYGVN-----RASVFPGLFNGTSPANGSGRDLYDDELPPDESI-- 465
 QY 403 LRCAFTARGSNYPDY-----FIRNISGVPLVY---RNEDLRRLAHNEIRNIESPS 453
 DB 466 ---GSSTRLSHTVFPSPQTNQAGSIANAGSVPTVYWRDVLNITITNRIITQLP--- 519
 QY 454 GTPGLRAVMSVANKNIYAVHNGTMHLAPEDYGTFTSPHATQVNNQTRTFISE 513
 DB 520 ---LVKA-----SAPVSGTVYKGG---GFI----- 539
 QY 514 KFGNQGDSLRFEOSNTTARTLRGNS---YNLYRVSSLGSTIRVTINGRYVYAS 568
 DB 540 ---GGILRTTNGTFG---TLRYVNSPLQRVRYVAFASGNFIRI-LRGNTSIAY 592
 QY 569 NAAVTNNDSVNDNGARFLDIMGVVASDNTVPLDINVT-----NSGT 614
 DB 593 QRFSGTNRG-----QELTVESFTSEFTTNSDLPFTTQAOENLTITLAEGVTS 644
 QY 615 QFLNIMFVPTN 627
 DB 645 EYFIDRIEIPVN 657

RESULT 2
 US-09-826-660-25
 Sequence 25, Application US/09826660
 Patent No. US20010026940A1
 GENERAL INFORMATION:

APPLICANT: Cardineau, Guy A.
 APPLICANT: Stelman, Steven J.
 APPLICANT: Naray, Kenneth B.
 TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins
 FILE REFERENCE: MA-714X2D1
 CURRENT APPLICATION NUMBER: US/09/826,660
 PRIOR FILING DATE: 2001-04-05
 PRIOR APPLICATION NUMBER: 09/178,252
 PRIOR FILING DATE: 1998-10-23
 PRIOR APPLICATION NUMBER: 60/065,215
 PRIOR FILING DATE: 1997-11-12
 PRIOR APPLICATION NUMBER: 60/076,445
 PRIOR FILING DATE: 1998-03-02
 NUMBER OF SEQ ID NOS: 27
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 25
 LENGTH: 643
 TYPE: PRT
 ORGANISM: Artificial Sequence
 OTHER INFORMATION: Toxin encoded by synthetic B.t. gene
 US-09-826-660-25

Query Match 9.2%; Score 305.5; DB 9; Length 643;
 Best Local Similarity 22.5%; Pred. No. 5e-19;
 Matches 142; Conservative 101; Mismatches 265; Indels 123; Gaps 25;

QY 52 PIVGTSSFLKKVSGSLGKRLSELWGLIPSGSTNLMODILRETEQFLNQRLNTDTLA 111
 DB 73 PFGQIVSFYSLVQ-----ELM-----PRG-RDPEHIEHVEDLIQVQNTENTD 118
 QY 112 RNVALEGLQANIREFNOQVDFNLTNPONVPLSTTSVNTMOQLFLNRLPQFVQ 170
 DB 119 TALARLOGLDSFNVQKSLQWMLADNDTRNLSVYRAQFIADLDVNAIFLFAVN 178
 QY 171 LILPLPAQANMLSFIDVVLNADWGISATLTQNTLYKNTTYSNCTINTYOTA 230
 DB 179 VPLIMVYAAQANMLHLRLDASLFGSEHGLTQGEISTYDQLELTKNTNCEWY 238
 QY 231 FRLG-NITRLHML---ERTYMFANVEYISWISFKYQSLVSSGANL---YASGSP 282
 DB 239 LNNIRKGNESWLRNQRFRDLTLGVLDVLPSTYTRVYPMNTSADLTREITDPIG 298
 QY 283 QOQTQS-FTSQDMPFLYSLFOVNSNYLVNGFSGARLTQTF-PNIGLPGTTTTALLAARV 340
 DB 299 TNAPSGFASGM-----FNNN---APSFALIAAVIRPHLPBPQLTFPSVLSRMS 348
 QY 341 NYSQGVSSGDIGAVFNQNFSCSTFLPLLTTPVNSW---LDGSGDRGVNTVN----- 391
 DB 349 N-----TOYMWVGHRLSERTIRGSLSTSTHGNTNT 380
 QY 392 ---WQTESPES-----TLGLRCAFTARGSNYPDYFIRNI--SG 427
 DB 381 SINVTLOFTSDVYRTRESFAGINILTTVPVNGVPMARFPMRPNLSLRGSLTYIGY 440
 QY 428 VPLVRENEDLRPLAHNEIRNIESPSGTGGLRAVMSVANKNIYAVHNGTMHLA 486
 DB 441 VGTQLPDSSTELPPTTERPNYESYSHRLSNR--LISGVTLLAPVSWITRRA----- 492
 QY 487 PEDYGTFTSPHATQV-----NQRTFISEKFGNQGDSLRFEOSNTTARTLRGNS 539
 DB 493 ---DRTN-TISSDSIQIPIVKSFNLSGTSVSGFGTGDDIIRTAVNSVLSMGLFNN 549
 QY 540 NS---YNLYRVSSLGSTIRVTING-RYTRASNVTNTTNDVNDNGARFLDIMGVVAS 595
 DB 550 TSLORRYRVRKAAQVTLRYVNGSTTFDQGPSTMSANESLTSQSFALRFPVGIS 609
 QY 596 ASDNTVPLDINVTNSGTO-FLNIMFVPTN 625
 DB 610 SGSGT---AGISISNNAQRQTFHDIETIP 637

RESULT 3

US-09-826-660-23
 ; Sequence 23, Application US/09826660
 ; Patent No. US20010026940A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cardineau, Guy A.
 ; APPLICANT: Stelman, Steven J.
 ; APPLICANT: Narva, Kenneth E.
 ; TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins
 ; FILE REFERENCE: MA-714XC2D1
 ; CURRENT APPLICATION NUMBER: US/09/826,660
 ; PRIOR FILING DATE: 2001-04-05
 ; PRIOR APPLICATION NUMBER: 09/1178,252
 ; PRIOR FILING DATE: 1998-10-23
 ; PRIOR APPLICATION NUMBER: 60/065,215
 ; PRIOR FILING DATE: 1997-11-12
 ; PRIOR APPLICATION NUMBER: 60/076,445
 ; PRIOR FILING DATE: 1998-03-02
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 23
 ; LENGTH: 1186
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Toxin encoded by synthetic B.t. gene
 ; US-09-826-660-23

Query Match 9.2%; Score 305.5; DB 9; Length 1186;
 Best Local Similarity 22.5%; Pred. No. 1,3e-18;
 Matches 142; Conservative 101; Mismatches 265; Indels 123; Gaps 25;
 52 PIVGVTSFLKKVSGILGRIISLMLGIFPSGSTMODILRETEQFLNRLNTDTLA 111
 73 PPAQGLASFSFLVG-----ELM-----PRG-RDPMWEIFLEHBOULINOITENARN 118
 112 RVNAEGLQANIRENQOVNFIPTQNPVPLSITSSVNTMOOL-FLNRLPQRFVQGY 170
 119 TALARLQGLDSFRAYQOQSLDWLENNRDARRSVLYTOYIALEDFLNAEFLAIRNOE 178
 171 LLLPLPQANMLHSIRDVLANDEWISATLRTQYQYKNTTYSYCNLYQTA 230
 179 VPLMWYQANLHLRLKRLASLFGSEFELTSQELQRYRYRQYKRETSYDCAKRWYNG 238
 231 FRGL-NTRLHML-EBRTYMLNFEVYSIMSLFFYQSLVSSGAML- YASGSGP 282
 239 LNNLRGTVAESWLRNQFRDLTLGLVLAFLPSYDTRYPMNTSAGLREIYTDIGR 298
 283 QQTQS-FTSQMPFLYSLFOVNSNYVLNGFSGARLTQTF-PNIGLPGTTTALLANV 340
 299 TNAISGFASITW-----FNNN-APSFALBAVAIRPPLDFFPOLTFISVLRWS 348
 341 NVSGGVSGDIGAVNQNFSCSTFLPPLITFPVRSW-----LDGSDRGVNTVN----- 391
 349 N-----TOYMWYWGRLHSRIRKSLSTHGWNT 380
 392 -----WQTESPES-----TLGRCGAPFARKNSNYPDYFIRNT-SG 427
 381 SINPVTLOFTSRDVRTESPAGINILITTPVNGVPMARFMRPRLNSLRGSLTYTGYG 440
 428 VPLVANEELRRPLHYEIRNIESPGTGGILRAYMVSVNRKNNTYA-VHEANGTMIHA 486
 441 VGTQLDSETELPEPETERPNYESYSHRLSNIR-LISGTLARAVYSWTHRSA----- 492
 487 PEDYGTFTSIPIATOVN-----NQRFTISKRENOQDLSAREGNTTARTYLRGNG 539
 493 --DRTN-TISSDSITQPLVYKSNLNGSVASGPGTGDITRTNVAGSLWGLNFPN 549
 540 NS---YNLYEVSLLNGSTIRYVING-RVYTAASVNTTNTNDGVNDNGARELDINNGNV 595
 550 TSLORRYRVRVYAAASQTMVLRVYVGSGTTFQGGPPTMSANSLNSGFRFAEPYGIS 609
 596 ASDNTNVPDLNVTENSGTQ-FELNMIMFVP 625

Db 610 SSGQT---AGISISNNAGROTTHFDKIEFIP 637

RESULT 4
 US-09-988-462-7
 ; Sequence 7, Application US/09988462
 ; Publication No. US20030046726A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kozziel, Michael G.
 ; APPLICANT: Desai, Nalini M.
 ; APPLICANT: Lewis, Kelly S.
 ; APPLICANT: Kramer, Vance C.
 ; APPLICANT: Warren, Gregory W.
 ; APPLICANT: Ewola, Stephen V.
 ; APPLICANT: Crossland, Lyle D.
 ; APPLICANT: Wright, Martha S.
 ; APPLICANT: Merlin, Ellis J.
 ; APPLICANT: Launis, Karen L.
 ; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
 ; INSECTICIDAL ACTIVITY IN MAIZE
 ; NUMBER OF SEQUENCES: 94
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Syngenta Biotechnology, Inc.
 ; STREET: 3054 Cornwallis Road
 ; CITY: Research Triangle Park
 ; STATE: NC
 ; COUNTRY: USA
 ; ZIP: 27709
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/988,462
 ; FILING DATE: 20-NOV-2003
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 09/547,422
 ; FILING DATE: 11-APR-2000
 ; APPLICATION NUMBER: US 08/459,504
 ; FILING DATE: 02-JUN-1995
 ; APPLICATION NUMBER: US 07/951,715
 ; FILING DATE: 25-SEP-1992
 ; APPLICATION NUMBER: US 07/772,027
 ; FILING DATE: 04-OCT-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Weigs, J. Timothy
 ; REGISTRATION NUMBER: 38,241
 ; REFERENCE/DOCKET NUMBER: S-188051
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (919)541-8687
 ; TELEFAX: (919)541-8689
 ; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1207 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
 ; US-09-988-462-7
 Query Match 8.3%; Score 275.5; DB 11; Length 1207;
 Best Local Similarity 21.9%; Pred. No. 7.4e-16;
 Matches 152; Conservative 98; Mismatches 226; Indels 217; Gaps 33;
 52 PIVGVTSFLKKVSGILGRIISLMLGIFPSGSTMODILRETEQFLNRLNTDTLA 111
 47 PPAQGLASFSFLVG-----ELM-----PRG-RDPMWEIFLEHBOULINOITENARN 92
 112 RVNAEGLQANIRENQOVNFIPTQNPVPLSITSSVNTMOOL-FLNRLPQRFVQGY 170
 93 TALARLQGLDSFRAYQOQSLDWLENNRDARRSVLYTOYIALEDFLNAEFLAIRNOE 152

QY 171 LLLPLFAOANMHLSPFRDVLVNADEMGISAALTQYNYLKNYTTSESNYCINTYOT- 229
 153 VPLMLVYAOANMHLSPFRDVLVNADEMGISAALTQYNYLKNYTTSESNYCINTYOT- 212
 QY 230 -AERGLN-----TRLDMLERFTYPLANEVYSIMSLFKYQSLVSSGANL-----YASG 279
 213 LNSLRGTNAAWVRVY---QFRDLTLGLVLDIALFSPYDRTPYINTSAQLTREYVYDA 269
 QY 280 SGPOQOSFTSQDM-----PFL-----YSLFQVNSVYLVNFGSGAR 315
 270 IGATGV-NMAMNMNNNNAPSESAIEAARSHLDELQTLTFSSSRW-----SMT 323
 QY 316 -----LTQPEPNIGLPGTTTHALLAARN-----YSGVSSGDI 351
 324 HMTYWRGHTIQSRPIGGGL--NTSGTATNTSINPVLTFASRDVYTESYAGVLMG-- 379
 QY 352 GAVFNQNFSCSTFLPPLLPFRSMIDSSDSRGVNTV---TWMQTESPESTLGLRGA 407
 380 -----TYLEPI-----HGVPTVRNFTPNQ----- 400
 QY 408 FTARGNSYPPDYFIRNISGVPLVYRNEDLRRLHAYNEIRNIESPSCPGGLRAYVSVH 467
 401 ISDRGTANYGOPY-----ESPLOIKDSFETLPETTERPYVESYSHR--LSHIGILLQ 452
 QY 466 NRKN-NIYA--VHENGTMHLAEDYTGFTSPHATOVNNGQTRTFIEKFGQGDLSRFE 525
 453 SHVNPVYSWTHSA-----DRTN-TIGPRKITQI---PMVAKSELQGTTV--- 495
 QY 526 QSNRTAARYLRNG--NSVNLVYRVSLSNSTIRVING-----RYTASVNTTT 574
 496 -----VRGPGFGDILIRKNTGPGPIRVNGLPQRYRIGFRYASTVDFEV 546
 QY 575 NNQDVNDGARFL-----DINMGVNV-----ASDVTNVP 604
 547 SGGGTNNRFLRTMNSGDELKGNVYRRAFTTPTFQIQDILRTSIGLSGNGEYI 606
 QY 605 D---INVTNSGTQPEL-----NMMEVPTN 627
 607 DKIELIPVATFEAEYDLERRAGAVNALFTNTN 639
 Db
 RESULT 5
 US-10-035-060-6
 ; Sequence 6, Application US/10035060
 ; Publication No. US2003040619A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Edwards, David
 ; APPLICANT: Wong, Siu-Yin
 ; APPLICANT: Hermsdorf, Corinna
 ; APPLICANT: Wilcox, Edward
 ; TITLE OF INVENTION: Process For Altering the Host Range Or Increasing The
 ; TITLE OF INVENTION: Toxicity Of
 ; TITLE OF INVENTION: Bacillus Thuringiensis Lepidopteran Toxins, and Recombinant DNA S
 ; FILE REFERENCE: M12CJPFJ3D1
 ; CURRENT APPLICATION NUMBER: US/10/035, 060
 ; PRIOR FILING DATE: 2001-12-27
 ; PRIOR APPLICATION NUMBER: US 08/580, 788
 ; PRIOR FILING DATE: 1999-09-27
 ; PRIOR APPLICATION NUMBER: US 08/580, 781
 ; PRIOR FILING DATE: 1995-12-29
 ; PRIOR APPLICATION NUMBER: US 08/420, 615
 ; PRIOR FILING DATE: 1995-04-10
 ; PRIOR APPLICATION NUMBER: US 08/097, 808
 ; PRIOR FILING DATE: 1993-07-27
 ; PRIOR APPLICATION NUMBER: US 07/980, 128
 ; PRIOR FILING DATE: 1992-11-23
 ; PRIOR APPLICATION NUMBER: US 07/803, 920
 ; PRIOR FILING DATE: 1991-12-06
 ; PRIOR APPLICATION NUMBER: US 07/356, 599
 ; PRIOR FILING DATE: 1989-05-24
 ; PRIOR APPLICATION NUMBER: US 06/904, 572

; PRIOR FILING DATE: 1986-09-05
 ; PRIOR APPLICATION NUMBER: US 06/808, 129
 ; PRIOR FILING DATE: 1985-12-12
 ; NUMBER OF SEQ ID NOS: 9
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 6
 ; LENGTH: 1177
 ; TYPE: PR
 ; ORGANISM: Bacillus Thuringiensis
 ; US-10-035-060-6
 Query Match 8.2%; Score 272; DB 15; Length 1177;
 Best Local Similarity 22.6%; Pred. No. 1.5e-15;
 Matches 158; Conservative 100; Mismatches 272; Indels 170; Gaps 29;
 QY 6 NNGRTTCANVVAHDPSEFHKSLDTRKEMWKRT--DHSIYVPIGVYSSFLK 63
 3 NNEPINEICIPYNCIS-----NPEVEVLGGERLETGYTPIDISL-----SLTPFLS 48
 Db
 QY 64 K---VGSIGRILSELMLGLIPSGSTNLMQDILRETEQFNLQRLNTDLARVNALEG 119
 49 EFPVAGFVLG--LVLDIKIGRPS-----QMDAFLVQIBQLNGRIIEEFARNOAISRLG 102
 QY 120 LQ-----ANIREPNOVDNFIPTQNPVPLSTSSVNTQQLNLNLPQFRVQGL 172
 103 LSNLYQIVASERFME-----ADPTNPALREEMKIQFNDMSALTTLAIPFAVNOYVP 156
 Db
 QY 173 LPLFAOANMHLSPFRDVLVNADEMGISAALTQYNYLKNYTTSESNYCINTYOTAFR 232
 157 LLSVYQOANMHLSPFRDVLVNADEMGISAALTQYNYLKNYTTSESNYCINTYOTAFR 216
 QY 233 ---GLNTRHML---EFTYPLANEVYSIMSLFKYQSLVSSGANLVYSSGPGQD 286
 217 RVWGPDSR--DWVRXNPFRELTLVLDIALFSP-----NYDSKRYPIRTY 260
 QY 287 SFTSDMPFLVSLPQVNSVYLVNFGSGA-----RLQTPENIGLPGTTTT 332
 261 SQLR-----EITNPVLENFDSFGSAQGISRSIRSPHMLDINSITLYTDAR 311
 Db
 QY 333 ---HALLAARNVSGVSS---GDIGAVFNQNFSCSTFLPPLLPFRSMIDSSG 381
 312 GYYWSGHQIMASPVGSGPEFTPLYGTMG---NAAIQRIYAOJGQGYTTLSTL 366
 Db
 QY 382 DRGQVTVNMQTESFESTGLRGAFTARGNSYPPDYFR-----NISGV-----L 430
 367 YRRPFIQINNQ-----QSVLDGTEFAYGSSNLBSAYRKSQTVDSINEIPQNNV 420
 QY 431 VVRNEDLRRLHAYNEIRNIESPSCPGGLRAYVSVNRK---NNIYVHE----- 478
 421 PPRQERSHLSSHVSFSGFSNSV-SIRAPFTSMQHRSAEPNNIISQITQIPILTS 479
 QY 479 ---NGTMHLAEDYTGFTSPHATOVNNGQTRTFIEKFGQGDLSRFGQSNRTAARY 534
 480 TNLGSGSVAKP---GFT-----GGDILR--RTSPQIS 510
 Db
 QY 535 LRGN-----GNSVNLVYRVSLSNSTIRVINGVYTAASVNTTTNNDQVNDGARFLDI 589
 511 LRVATTPLSQRYRKRIRYASTNLDLPHSISDGRPNQGFSTKSS--GSLNQGSGFRV 569
 QY 590 NMGNVVASDNTVPLDINV--TENSQTFQELNMMEVPTN 628
 570 GFTTPEFVNSGSSVFTLSAHVFNSGNEVYIDRIEVPDAEV 609
 Db
 RESULT 6
 US-10-032-717-8
 ; Sequence 8, Application US/10032717
 ; Publication No. US20020151709A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Andre R. Abad
 ; APPLICANT: Nicholas B. Duck
 ; APPLICANT: Xiang Feng
 ; APPLICANT: Ronald D. Flanagan

```

; APPLICANT: Theodore W. Kahn
; APPLICANT: Lynn B. Sims
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1 Proteins With
; TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
; FILE REFERENCE: 35718/237005
; CURRENT APPLICATION NUMBER: US/10/032,717
; CURRENT FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/242,838
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 667
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis (truncated)
US-10-032-717-8

```

Query Match	8.1%;	Score 269.5;	DB 14;	Length 667;
Best Local Similarity	22.7%;	Pred. No. 1e-15;		
Matches 135;	Conservative 91;	Mismatches 221;	Indels 147;	Gaps 24

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Qy 53 VGVGVSSPL-LKKVSGIGKRIILSELWCLTFPBGSGSNLMQOILAEFEQGLNORLMDTTLA 111
Db 76 IVGLKLSGSGVPFGPPIVVS--LYTQILDIMPSGQSGQWELFMEOVEELINKLAEYARN 133
Qy 112 RVNALESLQANIEEFNOQVDFNL-NTFONPVELSITSSVNTVMQOLFNLRLPFRFVGVGYO 170
Db 134 KALSELBEGIGNNYOULYTLALFEEMKENPFGSRLARDVRNFEILDSLFTYMPESFRVTFNE 193
Qy 171 LLLPLPFAAANMELSTIRVVLVANDENGSAATLTETVONTLKNYITEVSNCLNTYQTA 230
Db 194 VPELVYVYTOANMHLHLLMDASIFGBEKGSGSTTINNYYDQMLTAEISDHCHAKWEYIS 253
Qy 231 FRGLN---TRLDMLFEFTYFLNLFVEYVSIWSLFTKYQSLVSSGANL---YASGSGE 282
Db 254 LAKLKGTSAKQWVYNQFREMFTLTVLDVVALFPNDTRFYMETAQOLTRFVYTDLGA 313
Qy 283 QQOTSFSDQWPLFLYSLFQVNSNYLVNFGSALJOTEPNIGLPGTTTHALLAAR--- 339
Db 314 VNNSJGSG--WYDAPRFQVIESSVI-----RPHVNDYITGLVYTOSSRISSAAYIR 365
Qy 340 -----VNSGCVSSGSDIGAVP--NQN-SCSTFLPPLLTFPRASWLDGSGDRGAVNTYT 390
Db 366 HMAHQISYHAI FSDNLIKQMGTONMHSSTFF-----DPL 402
Qy 391 N--WQTESFESTLGLRCGAFARNSNVPPDY-FIRNISGVP-----LVARNEDLARPL 441
Db 403 NYDIYKTLKSAVL-----LDIVPEGTYI--FRGMPVEFPRVYNQNLNNTKTL 449
Qy 442 HYNELR-----NIESPS-----GTGGLRAYMVSVH 467
Db 450 KYNPASKOIIAGTRDSELELPETSDOPNYESHRLCHITSLPATGSTTGLGVLVFPEWTH 509
Qy 468 NRRKNIVYAVHENG-TML-----HLAPF-----DYTGFT-----ISPILHTQVNNQ 506
Db 510 RASADILNAVHSDKITQTPVVKVSDLAPSLGFGNNNTVVSGBGFTGGIILKVIKNGVLIHS 569
Qy 507 TRFFIEKFGNQGSLAEFQSTY-----ARTTL-RNGKSNVLY 545
Db 570 MRKYSIDINKEYSNRLKVASANNTEFYINDEENVKSHAQCTNMRDEALTNNPK 623

```

US-10-032-717-18
RESULT: 7
Sequence 18 Application US/1003271
Publication No. US20020151709A1
GENERAL INFORMATION:
APPLICANT: Andre R. Abad
INVENTOR: Nicholas B. Duck
APPLICANT: Xiang Feng
INVENTOR: Ronald D. Flanagan
APPLICANT: Theodore W. Kahn
INVENTOR: Lynn E. Sims

```

? TITLE OF INVENTION:  Genes Encoding No. US20020151709A1L Proteins With
? TITLE OF INVENTION:  Pesticidal Activity Against Coleopterans
? FILE REFERENCE: 35718/227005
? CURRENT APPLICATION NUMBER: US/10/032,717
? CURRENT FILING DATE: 2001-10-23
? PRIOR APPLICATION NUMBER: 60/242,838
? PRIOR FILING DATE: 2000-10-24
? NUMBER OF SEQ ID NOS: 48
? SOFTWARE: FastSeq, for Windows Version 4.0
? SEQ ID NO 18
? LENGTH: 673
? TYPE: PRT
? ORGANISM: Bacillus thuringiensis (truncated)
? US-10-032-717-18

```

Query Match	8.1%;	Score 269.5;	DB 14;	Length 673;
Best Local Similarity	22.7%;	Pred. No. 1.1e-15;		
Matches 135;	Conservative 91;	Mismatches 221;	Indels 147;	Gaps 24.

[illegible]

RESULT 8
 US-10-032-717-4
 Sequence 4, Application US/10032717
 Publication No. US20020151709A1
GENERAL INFORMATION:
 APPLICANT: Andre R. Abad
 APPLICANT: Nicholas B. Duck
 APPLICANT: Xiang Feng
 APPLICANT: Ronald D. Flanagan
 APPLICANT: Theodore W. Kahn
 APPLICANT: Lynn E. Sims
TITLE OF INVENTION: Genes Encoding No. US20020151709A1 Proteins With
 Pesticidal Activity Against Coleopterans

```

: FILE REFERENCES: 35718/237005
: CURRENT APPLICATION NUMBER: US-10-032,717
: CURRENT FILING DATE: 2001-10-23
: PRIOR APPLICATION NUMBER: 60/242,838
: PRIOR FILING DATE: 2000-10-24
: NUMBER OF SEQ ID NOS: 48
: SOFTWARE: SeqSeq for Windows Version 4.0.
: SEQ ID NO 4
: LENGTH: 1210
: TYPE: PR1
: ORGANISM: Bacillus thuringiensis
: US-10-032-717-4

```

Query Match	8.1%;	Score 269.5;	DB 14;	Length 1210;
Best Local Similarity	22.7%;	Pred. No. 2.6e-15;		
Matches 135;	Conservative 91;	Mismatches 221;	Indels 147;	Gaps 24;

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OY 53 IVGVSSFFL-LKKVOSLIGKRILSELMLGIFPSSSTYLMODILRETFOPFNOGLNDTLA 113
Db 76 IVGLDLSGLGPPVPGPIYS--LYTQULIDLWSSQSGMCEIMQEYBELNOKIMAYARN 133
OY 112 RVAAELEGLOANIREFNOQVDNFL-NPTONPVPLSTSSVNTMQLFLNRLPOFRYQO 170
Db 134 KASLEBEGGNNOYUJLTALEWKEKNPNRSALRDVNRREILDELFTQVPSFRVTYFE 193
OY 171 LLLLPLPAOANMHLSFBJADVLANDEMISATLFTQVYUKANTTESYSCINITYCPA 23
Db 194 VPELITVYTOANMLHLLILKODASIFGEBKMSTTTINNYDRQMLTAEDHCVKMYEFG 255
OY 231 FPGLN-----TRLHDLERRTYMPLANFEVYSIMSLFRYQSLVSSGANL-----YASGSP 287
Db 254 LAKKGTSAKOWMDVNOGRREMTLTYLDVVALFBNYTRTYRPMETKQALTRREYTDPLGA 313
OY 283 QOTOSFSPQDMPFLSLFOVNSNYVLNGFSGARLTQFPPIGGLPGTTTHALIAA--- 335
Db 314 VNVSISIS--WDXAPSGVIESSVI-----RPHNFEDITGLVVTYQMSISASRYR 365
OY 340 -----VNISGGVSGDIDGAVF--NONF-SCSTFLPPLLPFRVSMWLDSSGDRGCVNTY 390
Db 366 HMAHGQISYHRJFSNNIIKQVYKTONMHSSTF-----DFT 407
OY 391 N--WQTESFEHTGLRGCAFTARGNSNFPDY-FIRNISGVP-----LVYREDELRLPL 441
Db 403 NYDILKTLSDANL-----LDIYFPGYTYI--PFGMBEYEPFMVNOJNTRKYL 445
OY 442 HYNELR-----NIBSP-----GPRGGLAANVSVH 467
Db 450 KYNVPSKODIIAGTRDSELELPPESSQPNYBESYHRLCHITSPATGYSGLVLPVPSWTH 506
OY 468 NRKNUNIAVHENG-TMI-----HLAPB-----DYTGFT-----ISPIHATOVNNO 506
Db 510 RASADLINAHVSDKTIQIPVYKVSIDLPSITGGPNNTVVSQPGTGAGIKIVIRNGVISH 565
OY 507 TRTISLSEKFNQDGLAREQSNNT-----AAYTL-RGNNSYNLY 545
Db 570 MKVVISIDINKEYSMBIRASANTTEFYINPSEENVKSHACKTNGEALTYNKF 623

```

US-09-756-643-2
Sequence 2, Application US/09756643
Patent No. US2010026939A1
GENERAL INFORMATION:
APPLICANT: Rice, Douglas
APPLICANT: Carozzi, Nadine
APPLICANT: Anderson, David
APPLICANT: Rajasekaran, Kamniah
APPLICANT: Rangan, Thirumala
APPLICANT: Yenofsky, Richard
APPLICANT: Iotsestein, Richard
APPLICANT: de Fremond, Annick
TITLE OF INVENTION: Insecticidal Cotton Plant Cells
FILE REFERENCE: S-16768E

```

:
: CURRENT APPLICATION NUMBER: US/09/756,643
:
: CURRENT FILING DATE: 2001-01-08
:
: PRIOR APPLICATION NUMBER: 08/218,697
:
: PRIOR FILING DATE: 1994-03-28
:
: PRIOR APPLICATION NUMBER: 07/759,969
:
: PRIOR FILING DATE: 1991-09-16
:
: PRIOR APPLICATION NUMBER: 07/274,452
:
: PRIOR FILING DATE: 1988-11-18
:
: PRIOR APPLICATION NUMBER: 07/122,109
:
: PRIOR FILING DATE: 1987-11-18
:
: NUMBER OF SEQ ID NOS: 6
:
: SOFTWARE: Patentltn Ver. 2.0
:
: SEQ ID NO 2
:
: LENGTH: 1155
:
: TYPE: prt
:
: ORGANISM: Bacillus thuringiensis
:
: US-09-756-643-2

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Query Match 8.1%; Score 268; DB 9; Length 1155;
Best Local Similarity 22.7%; Pred. No. 3.3e-15;
Matches 159; Conservative 99; Mismatches 272; Indels 170; Gaps 29;

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0Y 6 NNGGTTICAYVVAHDPFSEHSLDITREKMMWKRT--DHLVAPVIGVSSFLK 63
Db 3 NNPINIECIPNYCS-----NPEVILGGERIERGVPIIDISL-----SLQFILS 48
0Y 64 K---VGSILGRILSLKMLLFPBSGSNNLMODILAEYHQLNQRNLMTDTLVAWAEIG 11.9
Db 49 EFWGAGFVLG--LVDTLWIKFQPS---QMDAFVLQIEQLNRIEERAKDALSREG 102
0Y 120 LQ-----ANIRENQOVNPLNPTONPVPLSTSSVNTWQOLNRLRQEPVQGYLL 177
Db 103 LSNLYQVASEPREME-----ADPTNRLAREEMRLQFDMNASLTLTALPLFVQNVQVP 156
0Y 173 LLPLPQAAHMHLEPFRIDVVLNADBMGSAALTRYQNTLKNYTTESNNCTNQTFR 232
Db 157 LLSTVYQAAHNLSTLVNDVSVGQKMGDAAITNSKYNLRLNGANTTBHARWNTBLE 216
0Y 233 ---GLNTRLHML---EERTYFPLNVPFYGSIMSLEKYSQSLVSSGANLYASGSPQTO 286
Db 217 RWMPBPSSR--DWIRNQFRRELTLVDIYSLP-----NDSTRYPRTV 260
0Y 287 SFTSQDMPLVSLFQVNSNVJLNGSGA-----RLTOTFPNIGLPGTTYT----- 332
Db 261 SQLR-----EYTNPLVLENFDGFSRGAQIEGIRSPHMLILMSITTYDNR 311
0Y 333 -----HALLAARVNSGVS-----GDIGAPNQNFSCTFLPPLLFPFRSMULDGS 381
Db 312 GEYWSGHQIMSPGSGSEFFPLPYTNM-----NAAPQRIVALQAGCYRTLSTL 366
0Y 382 DRGVNTVTNMQTESFESTJGLRCGAFTRAGNSNYFPDYFR-----NISGVLEVNE 435
Db 367 YRRFPNIGINNQ-----QLSVLDGTEFAYGTSNLSPAVYRKSGTVDSDLEIPQNNNV 420
0Y 436 DLR-----PLHYNEIRNISPEGTPGGLRXYWVYSHANK--NNIYAAHE----- 478
Db 421 PPRQGSRHLSVMSRFGSGNSSV-SIIRAPFMSIHSAEPNNILPSSQITQPLKRS 479
0Y 479 ---NGTMHLAPEDYGTFTSPFHATOVNNQRTTISEKFGQDLSLPEQGSNTTAYT 534
Db 480 TNLQSGSVVKGPP--GFT-----GQDILR--RTSPQIST 510
0Y 535 LRGN-----GNGVNYLRYVSSLSQSTIRVTLNGSVYTAASVNTTNDGVNDGARFLDI 589
Db 511 LRNVITAPLSQYKRRRLKRASTTNLQFHTSIDGRPLNGQNPALMTSS--GSNLQSGSFTV 569
0Y 590 NMGNVVASDNTNVPDLNV--TRNSGTQELMNLNMFPTUL 628
Db 570 GFTTTPFNFGSSVFTLSAHVFNSGAEVYIDRLBFPVPAEV 609

```

RESULT 10
US-09-988-462-5

Sequence 9, Application US/09988462
Publication No. US20030046726A1
GENERAL INFORMATION:

APPLICANT: Koziel, Michael G.

Deesai, Nalini M.

Lewis, Kelly S.

Kramer, Vance C.

Warren, Gregory W.

Evola, Stephen V.

Crossland, Lyle D.

Wright, Martha S.

Merlin, Ellis J.

Launis, Karen L.

TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED

NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS: 94

ADDRESSEE: Syngenta Biotechnology, Inc.

STREET: 3054 Cornwallis Road

CITY: Research Triangle Park

STATE: NC

COUNTRY: USA

ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/988,462

FILING DATE: 20-NO. US20030046726A1-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/547,422

FILING DATE: 11-APR-2000

APPLICATION NUMBER: US 08/459,504

FILING DATE: 02-JUN-1995

APPLICATION NUMBER: US 07/951,715

FILING DATE: 25-SEP-1992

APPLICATION NUMBER: US 07/772,027

FILING DATE: 04-OCT-1991

ATTORNEY/AGENT INFORMATION:

NAME: Weigert, J. Timothy

REGISTRATION NUMBER: 38,241

REFERENCE/DOCKET NUMBER: S-188051

TELECOMMUNICATION INFORMATION:

TELEPHONE: (919) 541-8587

TELEFAX: (919) 541-8689

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 1155 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 9:

US-09-988-462-9

Query Match

Best Local Similarity 22.7%; Score 268; DB 11; Length 1155;

Matches 159; Conservative 99; Mismatches 272; Indels 170; Gaps 29;

QY 6 NNGRTTICDANYVAHDPSPFEHKSLLDTIRKEMMEKRT--DHSLYVAPIGVVSSFLIK 63

DB 3 NNPNINCEIPYNCLT-----NPEVEVLGGERIEGVTPIDISL-----SLTPFLIS 48

QY 64 K-----VSLIKRIISLMLGLIFPSGSTNLMQDILAEFGQPLNQLNTTTLARVNAELRG 119

DB 49 EKVVGAGFVLG--LVDTITMGIFGFS---QMDAFVQLIBOLINQRIEFPARNOALSREG 102

QY 120 LQ-----ANIEFNQOVNPLNPTONPVPLSTISSVNTVQQLFLNRLPFRVVOGYQL 172

DB 103 LSNLYQIYASFRFEME-----ADPTNPALREMRIGFNDNNSALTATAPLFAVQNYVP 156

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/547,422

QY 173 LLEPFAOAMNHLSPIRDVYVNADEKGLSAATLRTYQNTLAKNTTETSNYCINTYOTAR 232

DB 157 LLSVYQAHNHLSSVRDVSFGQKMGDAATINSKNDLRLIGNYTLDAVAVMYTGLE 216

QY 233 ---GLNTRLDML---EFTYVFLNVEEYVSIWLEKYQSLVSGANLAYSQSGPQTO 286

DB 217 RVWGFDSE--DWIRYQFRELTLVLDIVSLP-----NDSRTYPIRV 260

QY 287 SFTSQDMWFLYSLFOVNSNYVANGSGA-----RLQTFPNIQGLPQITTT 332

DB 261 SOLTR-----EYTPVLENDSFPGSAQIGIESINSLHMDIINSLITTYDAHR 311

QY 333 -----HALLAARVNSGVNS-----GDGAVFNQNSCSFTPLPLTFYASWLDGSS 381

DB 312 GRYVSGHQIMASPVVFGSGEFTFPYGTWG-----NAPQORIVAGQGVYRTLSLT 366

QY 382 DGGVNTVTWQTESFESTLGLRCGAFATAGNSNYPDYFIR-----NISGVLVYNE 435

DB 367 YRPPNIGINN-----QSLVDGTFEPAVGTSSNLPANVYRKSGTVDSLDRIIPQNNV 420

QY 436 DLK-----PFLHYNEIRNIESPSGTGGLRAYVSVNHRK---NNIYVHE----- 478

DB 421 PPGQFHRHLSHVMRSGFSNSV--SIRAPWFMIHRSALFPNNIIPSSQITQIPLTKS 479

QY 479 ---NGTMIHAPEDYGTFTSPIHATOVNQTFTFIEKFGNGGSLFPEQSNNTAYT 534

DB 480 TMLSGTSVYKGP---GFT-----GGDLR--RTSPGQIST 510

QY 535 LRGN-----GNSNYLYRVSLSNSTRTVINGRYVTAENVNTTNDGVNNGARPLDI 589

DB 511 LRVTAPLSQRYRVARIRASTTLMOPHTSIDGRINDGNSATMS--GSLNQSFPRTV 569

QY 590 IMGNVVASDNTVPLDINV--TFNSGTQFELNMIMVPTNL 628

DB 570 GTTPPFNSGSSVFTLSAHVFNAGNEVYIIDEVPAV 609

RESULT 11

US-09-988-462-11

Sequence 11, Application US/09988462

Publication No. US20030046726A1

GENERAL INFORMATION:

APPLICANT: Koziel, Michael G.

Deesai, Nalini M.

Lewis, Kelly S.

Kramer, Vance C.

Warren, Gregory W.

Evola, Stephen V.

Crossland, Lyle D.

Wright, Martha S.

Merlin, Ellis J.

Launis, Karen L.

TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED

NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS: 94

ADDRESSEE: Syngenta Biotechnology, Inc.

STREET: 3054 Cornwallis Road

CITY: Research Triangle Park

STATE: NC

COUNTRY: USA

ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/988,462

FILING DATE: 20-NO. US20030046726A1-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/547,422

Fri Aug 15 11:51:35 2003

us-10-040-906a-2.rapb

Page 8

FILING DATE: 11-APR-2000
APPLICATION NUMBER: US 08/459,504
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Weiger, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-188051
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1181 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-988-462-11

Query Match 8.1%; Score 268; DB 11; Length 1181;
Best Local Similarity 22.7%; Pred. No. 3.5e-15;
Matches 159; Conservative 99; Mismatches 272; Indels 170; Gaps 29;

6 NNGRTTICDANYVAHADPFSEHKSLDTRKEMEMKRT--DHSLYAPVIGTVSSFLK 63
3 NNPINIECTPYNCL-----NPEVEVLGGERIETGYTPIDSL-----SLTQPLLS 48
4 K---VGSILGRITSELMGLIFPSGSNTLMODILRETEQFNLQRLNTDLARVNAELRG 119
49 EFPVAGAFVIG--LVDIIMGIFGPS-----QMDAFVQIEQLINQRIEFAFNQAIISRLRG 102
120 LQ-----ANIRENQVDNFMFLPQNPVPLSTSSVNTMQLFLNRLPORVQVQL 172
103 LSNLYQIVASEPFEWE-----ADPTNPALREEMRIOPDNNSALFTTALPFAVNTQVP 156
173 LPLPFAQANMHLSPFRDVLNADMGISATLRTYQNYLKNYTTESYNCINYQVAFR 232
157 LLSVYQANMHLSTLRDVSFQGRKGFDAITNSRNDLRLIGNVTDHVRWVNGLE 216
233 ---GLNTRLDML--ERTTMEPLNVEYVSTMSLFXQSLVSSGAMLYAGSGPQQTQ 286
217 RWMGPDSR--DMIRNQFRRELTLTVLDIVSLFP-----NDSRTPLRIV 260
287 SFTSQDMPFLYSLFQVNSNYVINGFSGA-----RLTQTFPNIGGLPQTITT----- 332
261 SGLR-----ELYNPVLNENFDSFPGSAQIGSIRSPLMDILNLSITITVDNR 311
333 -----HALLARVNYSGVSS-----GDIQANFQNSGCTPLPPLPFPVRSWLDGSG 381
312 GEYWSGHQIMASPVFSGPEFTPLXGTNG-----NAPQQRIVAGQGYRTLSL 366
382 DRGQNTVTVMQTESPEFTLGRCAFTARGNSNYPDYFR-----NISGVPLVENE 435
367 YRRPNTGIGNN-----QLSYLDGTEFAVGTSSNLSAVYRKSGIVDSIDEIPQNNNV 420
436 DLK-----RLPAYNEIRNIESPGTGGLAAYVSVNHRK-----NNIYAVHE----- 478
421 PPRQGFHRLSHVSMRSGFSNSV--SIIPAFSVIHRSAFPNNIIPSSQITQPLRKS 479
479 ---NGTMILAPEDYTGFTSPIHATQVNNQRTFRISBFGNQGSLRPEGSNTTART 534
480 TWLGSQTSVAKGP-----GFT-----GGDILR--RTSGQIST 510
535 LRGN-----GNSYNLVARISLNGSTIRVTINGRVYTAANVTITNDGVNDGARFPDI 589
511 LKVNITLAPLSQRTYRIRASTTNLQHTSIDRPLINQNSFSAIMS--GSNLSGSRFTV 569
590 NMGNVVASDNTNVPDLINV--TNSGTOFELNIMFPVITNL 628

DB 570 GFTTPEFNSGSSVFTLSAHVNSGNEVYIDRIEFVPAEV 609

RESULT 12
US-09-988-462-13
Sequence 13, Application US/09988462
Publication No. US20030046726A1
GENERAL INFORMATION:
APPLICANT: Koziel, Michael G.
Desai, Nalin M.
Lewis, Kelly S.
Kramer, Vance C.
Watten, Gregory W.
Evola, Stephen V.
Crosland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Laudis, Karen L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESS: Syngenta Biotechnology, Inc.
STREET: 3054 Cornwalis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/988,462
FILING DATE: 20-NOV-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/547,422
FILING DATE: 11-APR-2000
APPLICATION NUMBER: US 08/459,504
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Weiger, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-188051
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 1181 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-988-462-13
Query Match 8.1%; Score 268; DB 11; Length 1181;
Best Local Similarity 22.7%; Pred. No. 3.5e-15;
Matches 159; Conservative 99; Mismatches 272; Indels 170; Gaps 29;

6 NNGRTTICDANYVAHADPFSEHKSLDTRKEMEMKRT--DHSLYAPVIGTVSSFLK 63
3 NNPINIECTPYNCL-----NPEVEVLGGERIETGYTPIDSL-----SLTQPLLS 48
4 K---VGSILGRITSELMGLIFPSGSNTLMODILRETEQFNLQRLNTDLARVNAELRG 119
49 EFPVAGAFVIG--LVDIIMGIFGPS-----QMDAFVQIEQLINQRIEFAFNQAIISRLRG 102

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QY 120 LQ-----ANIRENQVNDPLNPTQNPVLSTSSVNTMQLFLNRLPOFRVQYQL 172
DB 103 LSNLYOIVASFRME-----ADPTNPALEKRIQFNOMNSALTALPLFAVQNV 156
QY 173 LPLPFAOANMHLSTFDVYVLANDEWIGISAATLRYQNYKATTEYSNYCINTYQAFR 232
DB 157 LLSVYQOANMHLSTFDVSVFGQRFDAATINSRNDLTRIGNYDHAVRMYNGLE 216
QY 233 ---GLNTRLHML---EFTYMFANFEVYSIWSLFFYQSLVSGANLYASGSGPOQTQ 286
DB 217 RWGPDNR--DWIRYNOFRRELTLYLDIVSLFP-----NYDSRYPIRYV 260
QY 287 SFTSQDMPFLVSLFOVNSVYLVNGPSGA-----RLTQTPNIGLPGCTTT----- 332
DB 261 SOLTR-----EITYNVLENFDSFRSQAQIEGSIKSPHLMIDINSITTYDAHR 311
QY 333 -----HALLAARVNSGVS-----GDIGAVENQFSCSTFLPPLTTPVSWLDSGS 381
DB 312 GEYWSGHQIMASVFGSGEPFLPYGTMG-----NAAPQRIVAQLGQGVRTLSSTL 366
QY 382 DRGVVYVYNNQTSFESTLGLRCGAFARNSNYPDYFIR-----NISGVPLVVRNE 435
DB 367 YRRPFGIGNQ-----QSLVDGTERFAYGTSNLSAVYKSGTVDSLDEIPQNNV 420
QY 436 DLK-----RPLATNEIRNIESPSGTPGGLAAYVSVHNR--NNIYAVH----- 478
DB 421 PRQGFSHRLSHVSMFSGFSNSV-SIIRAPMFSWIRHSAFNNTIPSSQITQILTKS 479
QY 479 ---NGTMIHLAPEDYGTISPPIHATQVNNQRTISKFNQDLSLRQSNNTART 534
DB 480 TWDGSGTVKGP-----GFT-----GDDIR--RTSPQIST 510
QY 535 LGN-----GNSYNULYRVSLGNSITRTVINGRVYASVNTTNDGVNDGARFLDI 589
DB 511 LKVNITAPLSORFVRIRYASTTNLQFHTSIDGRPINQGNFATWSS--GSLQSSGFRIV 569
QY 590 NMGVNVASDNTVPLDIN--TENSQTOPELIMNIFVPTL 628
DB 570 GTTPEFNSGSSVFTLSAHVNSGNVYIDRIEFPAV 609

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RESULT 13

US-09-988-462-15
 Sequence 15, Application US/09988462
 Publication No. US20030046726A1
 GENERAL INFORMATION:

APPLICANT: Kozel, Michael G.

Debat, Nalin M.

Lewis, Kelly S.

Kramer, Vance C.

Warren, Gregory W.

Evola, Stephen V.

Crossland, Lyle D.

Wright, Martha S.

Merlin, Ellis J.

Launis, Karen L.

TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED

NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:

ADDRESSEE: Syngenta Biotechnology, Inc.

STREET: 3054 Cornwallis Road

CITY: Research Triangle Park

STATE: NC

COUNTRY: USA

ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

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APPLICATION NUMBER: US/09/988,462
FILING DATE: 20-NO. US20030046726A1-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/547,422
FILING DATE: 11-APR-2000
APPLICATION NUMBER: US 08/459,504
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Weigs, J. Timothy
REGISTRATION NUMBER: 38,241
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 1181 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-988-462-15

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Query Match 8.1%; Score 268; DB 11; Length 1181;
 Best Local Similarity 22.7%; Pred. No. 3.5e-15;
 Matches 159; Conservative 99; Mismatches 272; Indels 170; Gaps 29;

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QY 6 NNGGTTICAVYVNDPFSFEKSLDITRKEMMKRT--DHSLYADIVCTVSSFLTK 63
DB 3 NNPINCEPIPCIS-----NEVEVLGGRILETYPIDISL-----SLQFILLS 48
QY 64 K---VSLIGKILSELMLIPSGSTNIMODILRETEQFLNQRINTDRLARVAELRG 119
DB 49 EFVAGAVFLG--LVLDIMGIFGFS---QMDAPLVQIBQLNQRLEEFARQAISRLG 102
QY 120 LQ-----ANIRENQVNDPLNPTQNPVLSTSSVNTMQLFLNRLPOFRVQYQL 172
DB 103 LSNLYOIVASFRME-----ADPTNPALEKRIQFNOMNSALTALPLFAVQNV 156
QY 173 LPLPFAOANMHLSTFDVYVLANDEWIGISAATLRYQNYKATTEYSNYCINTYQAFR 232
DB 157 LLSVYQOANMHLSTFDVSVFGQRFDAATINSRNDLTRIGNYDHAVRMYNGLE 216
QY 233 ---GLNTRLHML---EFTYMFANFEVYSIWSLFFYQSLVSGANLYASGSGPOQTQ 286
DB 217 RWGPDNR--DWIRYNOFRRELTLYLDIVSLFP-----NYDSRYPIRYV 260
QY 287 SFTSQDMPFLVSLFOVNSVYLVNGPSGA-----RLTQTPNIGLPGCTTT----- 332
DB 261 SOLTR-----EITYNVLENFDSFRSQAQIEGSIKSPHLMIDINSITTYDAHR 311
QY 333 -----HALLAARVNSGVS-----GDIGAVENQFSCSTFLPPLTTPVSWLDSGS 381
DB 312 GEYWSGHQIMASVFGSGEPFLPYGTMG-----NAAPQRIVAQLGQGVRTLSSTL 366
QY 382 DRGVVYVYNNQTSFESTLGLRCGAFARNSNYPDYFIR-----NISGVPLVVRNE 435
DB 367 YRRPFGIGNQ-----QSLVDGTERFAYGTSNLSAVYKSGTVDSLDEIPQNNV 420
QY 436 DLK-----RPLATNEIRNIESPSGTPGGLAAYVSVHNR--NNIYAVH----- 478
DB 421 PRQGFSHRLSHVSMFSGFSNSV-SIIRAPMFSWIRHSAFNNTIPSSQITQILTKS 479
QY 479 ---NGTMIHLAPEDYGTISPPIHATQVNNQRTISKFNQDLSLRQSNNTART 534
DB 480 TWDGSGTVKGP-----GFT-----GDDIR--RTSPQIST 510
QY 535 LGN-----GNSYNULYRVSLGNSITRTVINGRVYASVNTTNDGVNDGARFLDI 589

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Db 511 LKVNITAPLSGRVVRIRYASTTNLQFHTSIDGRPIINGNFSATWSS-GSNLQSGSFRTV 569
 Qy 590 NMGNVVASDNTNVPDLINV-TENSGTOPELNMIMFVPTNL 628
 Db 570 GFTTPEFNPSNGSVFTLSAHVFNNSGNEVYIDRIEFVPAEV 609

RESULT 14

US-09-988-462-17
 Sequence 17, Application US/09988462
 Publication No. US20030046726A1

GENERAL INFORMATION:

APPLICANT: Kozziel, Michael G.
 Desai, Nalini M.
 Lewis, Kelly S.
 Kramet, Vance C.
 Warren, Gregory W.
 Evola, Stephen V.
 Crossland, Lyle D.
 Wright, Martha S.
 Merlin, Ellis J.
 Launis, Karen L.

TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
 INSECTICIDAL ACTIVITY IN MAIZE

NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:

ADDRESSEE: Syngenta Biotechnology, Inc.
 STREET: 3054 Cornwallis Road
 CITY: Research Triangle Park
 STATE: NC

COUNTRY: USA

ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/988,462

FILING DATE: 20-NO. US20030046726A1-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/547,422

FILING DATE: 11-APR-2000

APPLICATION NUMBER: US 08/459,504

FILING DATE: 02-JUN-1995

APPLICATION NUMBER: US 07/951,715

FILING DATE: 25-SEP-1992

APPLICATION NUMBER: US 07/772,027

FILING DATE: 04-OCT-1991

ATTORNEY/AGENT INFORMATION:

NAME: Melgs, J. Timothy

REGISTRATION NUMBER: 38, 241

REFERENCE/DOCKET NUMBER: S-188051

TELECOMMUNICATION INFORMATION:

TELEPHONE: (919)541-8587

TELEFAX: (919)541-8689

INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:

LENGTH: 1181 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 17:

US-09-988-462-17

Query Match 8.1%; Score 268; DB 11; Length 1181;
 Best Local Similarity 22.7%; Pred. No. 3.5e-15;
 Matches 159; Conservative 99; Mismatches 272; Indels 170; Gaps 29;
 6 NNGRTTICDAVNVAVADPFSFEHKSIDTIRKEMWEMKRT--DHSLYVAPIVGTSSFLIK 63

Db 3 NNPINICEIPYNCLS-----NPEVEVLGGERIETGYTIDISL-----SLTQFLIS 48
 Qy 64 K---VGSILGRITSLMGLIFPSSGNTLMODILRETEQFLNORLNTDLARVNAELRG 119
 Db 49 EFPVGAEPVAG--LVDITWIGFPGS---QMDAPLVQIEQLINQREEPARNAQASISLEG 102
 Qy 120 LQ-----ANIREPNOQVDFNLPQNPVPLISTSSVNTMQLFLNRLPOFRVQVOLL 172
 Db 103 LSNLYQIYVASEPREWE-----ADPTNPALREEMKIOFNMDNSALTATLPLFAVQNTQVP 156
 Qy 173 LLEPFAQANMHSFIRDPVNLADENGISAATIRTYQVYLNKNTYTESVNYCINTYQTAFR 232
 Db 157 LLSVYVQANLHSLVRKDVSVFGQKMGFPDATTINRYVDLRLIGNYTDHVAWMYNTGLE 216
 Qy 233 ---GIATRLDML---EERTYMLANFEYVSTWSLFFKQSLIVSSGAMNLYASGSPQQTQ 286
 Db 217 RVMGPDSS--DWIRYQFRRELTLVLDIVSLFP-----NYSRTYPIRTV 260
 Qy 287 SFTSQDMPFLYSLFOVNSNYLVNGFSGA-----RLTQTPNIGLPGTTLT----- 332
 Db 261 SGLTR-----EITYNPLENFDSFRGSAQIEGSIKSPHMDILNSITTYTDAAHR 311
 Qy 333 -----HALLARVNYGGSV---GDIQAVFNQNSCSTFLPLTPFVRSLDSCS 381
 Db 312 GRYWSGHQIMASPVGSGPEFTPIYGTWG-----NAPQQRIVAQLOGGYRLSSTL 366
 Qy 382 DRGVNTVTNMQTESPESTLGLRCGAFIARGNNSYPPDYFIR-----NISGVLVANE 435
 Db 367 YRPNPNGINQ-----QLSVLDGTFAVGTSSNLPFAVRKSGTVDSIDELPPQNNNV 420
 Qy 436 DLR-----RPLHNEIRNIESPGTGGALAYVSVVHRK---NNIYAVIE----- 478
 Db 421 PPRQGFSLRSHVSMRSGFSNSV-SIIRAPMFWIRHSAFNNIIPSSQITQIPLRKS 479
 Qy 479 ---NGTMIHAPEDYTGFTISPIHATOVNNQRTFISEKGNQDGLAREQSNNTARTY 534
 Db 480 TULSGTSVVGCP---GFT-----GGDILR--RTSPQIST 510
 Qy 535 LKGN-----GNSVNLKARVSLGNSITRTVINGRYVYASNVYTTNNDGVNDGARFLDI 589
 Db 511 LKVNITAPLSGRVVRIRYASTTNLQFHTSIDGRPIINGNFSATWSS-GSNLQSGSFRTV 569
 Qy 590 NMGNVVASDNTNVPDLINV-TENSGTOPELNMIMFVPTNL 628
 Db 570 GFTTPEFNPSNGSVFTLSAHVFNNSGNEVYIDRIEFVPAEV 609

RESULT 15

US-09-988-462-28

Sequence 28, Application US/09988462

Publication No. US20030046726A1

GENERAL INFORMATION:

APPLICANT: Kozziel, Michael G.
 Desai, Nalini M.
 Lewis, Kelly S.
 Kramet, Vance C.
 Warren, Gregory W.
 Evola, Stephen V.
 Crossland, Lyle D.
 Wright, Martha S.
 Merlin, Ellis J.
 Launis, Karen L.

TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
 INSECTICIDAL ACTIVITY IN MAIZE

NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:

ADDRESSEE: Syngenta Biotechnology, Inc.
 STREET: 3054 Cornwallis Road
 CITY: Research Triangle Park
 STATE: NC

COUNTRY: USA

ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION NUMBER: US/09/988,462
 FILING DATE: 20-NOV-2003
 CLASSIFICATION: US20030046726A1-2001
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 09/547,422
 FILING DATE: 11-APR-2000
 APPLICATION NUMBER: US 08/459,504
 FILING DATE: 02-JUN-1995
 APPLICATION NUMBER: US 07/951,715
 FILING DATE: 25-SEP-1992
 APPLICATION NUMBER: US 07/772,027
 FILING DATE: 04-OCT-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Weigs, J. Timothy
 REGISTRATION NUMBER: 38,241
 REFERENCE/DOCKET NUMBER: S-188051
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (919) 541-8587
 TELEFAX: (919) 541-8689
 INFORMATION FOR SEQ ID NO: 28:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1181 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 28:
 US-09-988-462-28

Query Match 8.1%; Score 268; DB 11; Length 1181;
 Best Local Similarity 22.7%; Pred. No. 3,5e-15;
 Matches 159; Conservative 99; Mismatches 272; Indels 170; Gaps 29;
 QY 6 NNGRTTICDANYVVAHDPFSEHKSIDTIRKEMWERT--DHSLYVAVIVGVSSFLK 63
 DB 3 NNPINIECIYFNCIS-----NPEVEVLGERIERGTYPIDISL-----SLQFLLS 48
 QY 64 K---VSLGKRIISLSELMGLIFPSGSTNLMODIARETEOFLNORLNTDTLARVNAELG 119
 DB 49 EIVPGAGFVIG--LVDIIMGIFPS---QMDAFVIOIEOLINQRIEFPARQAISRLEG 102
 QY 120 LQ-----ANIREFNOQVDNPLNPTQNPVPLSITSSVNTWQQLFLNRLPOPRVQYQL 172
 DB 103 LSNLYQIYASPREME-----ADPTNPALREEMRIQFNDKNSALTTAIPFAVONYQVP 156
 QY 173 LLEPLQAAMHLSPIRQVLANADEKGISATLRTYONYLVNNTTEYSNYCINTYQTAFR 232
 DB 157 LLSVYVQAANLHLSVLRDVSFVGQRMGFMAATINRYNDLTRLIGNYTDHAAVRWYNGLE 216
 QY 233 ---GLNTRLMDL---EFFRYMFLNFEVYSIMSLFKYQSLVSSGANLYASGSGPOQTQ 286
 DB 217 RVWGPDSDR--DWIRYNQFRRELTLTVLDIVSLP-----NYDSRTYPIRTV 260
 QY 287 SFTSQDMPLFVSLFQVNSNYVLANFGSA-----RLQTFPNIGALPGTTT----- 332
 DB 261 SQLTR-----EITNPVLENFDSFRGSAQIGSIRSPHMDIINSITTYTDAHR 311
 QY 333 -----HALLAARVNSGVSS---GDIGAVFNQNFSCSTFLPPLTFPFRSMDSGS 381
 DB 312 GEYYSQHOIMASPVGFSGPEFTFPLYGTMG---NAAPQQRIVAQLOQGVYRTLSSTL 366
 QY 382 DRGGVNTVNMQTESFESTLGLRGAFTARGNSNFPDYFIR-----NISGVPLVVRNE 435
 DB 367 YRRFNIQINNO-----QLSVLDGTERFAYGTSSNLPBAYVRKSGTVDLDEIPQNNNV 420
 QY 436 DLR-----RPLHNEIRNISPSGTGGLRAYVSVNHRK---NNIYAVHE----- 478
 DB 421 PPOGFSHRLSHVSMFRSGFSNSSV--SIRAPMFMIHRSAEFNNIIPESQITQIPLTKS 479

QY 479 ----NGTMHLAPEDYTGTSPIHANQVANNQRTFIFISKFGNOGDSLRFEGSNTTART 534
 DB 480 TNLGSGISVVKGP---GFT-----GGDILR--RTSPQOIST 510
 QY 535 LRGN-----GNSYNYLIRVSLGNSITRTVINGRVYTASVNTTNNNDGVNDGARPLDI 589
 DB 511 LRNVITAPLSQRVRYRIRYASTTNLQPHISIDGRPLINGNSFATMS--GNSLQSGSFRTV 569
 QY 590 MNGAVVASDNTNVPDIDNV--TPNSGTQFELAMINMEVPTNL 628
 DB 570 GTTTPNFNSGSSVFTLSAHVFNSGNEVYIDRIEFVPAEV 609

Search completed: August 14, 2003, 18:14:02
 Job time : 37 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 14, 2003, 18:09:22 ; Search time 27 Seconds
(without alignments)
2251.060 Million cell updates/sec

Title: US-10-040-906a-2

Perfect score: 3314

Sequence: 1 MNVYVNGRTTICDANVVA.....GTQELMIMFVPTNLEPIY 632

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: PIR 76:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3048.5	92.0	633	2 C32053	paraaporal crystal
2	3010.5	90.8	633	2 D32053	paraaporal crystal
3	2545	76.8	622	2 S17402	paraaporal crystal
4	336.5	10.2	643	2 A43647	paraaporal crystal
5	327.5	9.9	719	2 I39815	insecticidal prote
6	324.5	9.8	719	2 S25383	paraaporal crystal
7	324.5	9.8	719	2 I39814	insecticidal prote
8	310.5	9.4	719	2 I40590	cryV465 protein -
9	307	9.3	1157	2 S49247	paraaporal crystal
10	294.5	8.9	1176	2 A48970	paraaporal crystal
11	282.5	8.5	1176	2 J70241	paraaporal crystal
12	280.5	8.5	934	2 A23798	paraaporal crystal
13	277.5	8.4	380	2 B42459	paraaporal crystal
14	277	8.4	1181	2 A41052	paraaporal crystal
15	276.5	8.3	1176	2 UC2219	paraaporal crystal
16	275.5	8.3	1228	2 S00873	paraaporal crystal
17	273	8.2	1155	2 A26513	paraaporal crystal
18	271.5	8.2	1176	2 A22617	paraaporal crystal
19	271.5	8.2	1176	2 S02215	paraaporal crystal
20	269	8.1	1155	2 S02134	paraaporal crystal
21	268	8.1	1155	2 J00002	paraaporal crystal
22	268	8.1	1156	2 A28125	paraaporal crystal
23	267.5	8.1	1178	1 US65X1	paraaporal crystal
24	267	8.1	1155	2 I39838	paraaporal crystal
25	265	8.0	1174	2 A42459	paraaporal crystal
26	264.5	8.0	1160	2 I40589	paraaporal crystal
27	264	8.0	1174	2 S32649	paraaporal crystal
28	262.5	7.9	1156	2 A29838	paraaporal crystal
29	261.5	7.9	1172	2 S32689	paraaporal crystal

30	259	7.8	1165	2 S11446	paraaporal crystal
31	259	7.8	1177	2 A45785	paraaporal crystal
32	255.5	7.7	649	1 JH0261	paraaporal crystal
33	253	7.6	618	2 S11445	paraaporal crystal
34	253	7.6	1138	2 A48944	paraaporal crystal
35	250	7.5	652	2 A27323	paraaporal crystal
36	249.5	7.5	652	2 I39811	paraaporal crystal
37	247.5	7.4	659	2 S10228	paraaporal crystal
38	244	7.4	1160	2 S32647	paraaporal crystal
39	237	7.2	613	2 UC6033	paraaporal crystal
40	230.5	7.0	655	2 UC7140	mosquitocidal prot
41	229.5	6.9	1189	2 S00944	paraaporal crystal
42	225	6.8	823	2 S04181	paraaporal crystal
43	218.5	6.6	1171	2 A37829	paraaporal crystal
44	218.5	6.6	1171	2 I40572	paraaporal crystal
45	216	6.5	1154	2 S39536	paraaporal crystal

ALIGNMENTS

RESULT 1

C32053

paraaporal crystal protein B1 - Bacillus thuringiensis subsp. kurstaki

N:Alternate names: paraaporal crystal protein P2

C:Species: Bacillus thuringiensis subsp. kurstaki

C>Date: 13-Jul-1989 #sequence_revision 13-Jul-1989 #text_change 15-Oct-1999

C:Accession: C32053; A29913

R:Midner, W.R.; Whiteley, H.R.

J. Bacteriol. 171, 965-974, 1989

A:Title: Two highly related insecticidal crystal proteins of Bacillus thuringiensis subsp.

A:Reference number: A32053; WUID:89123178; PMID:2914879

A:Accession: C32053

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-587, 'PRV' <DON>

A:Molecule type: DNA

A:Residues: 1-587, 'PRV' <DON>

A:Molecule type: DNA

A:Residues: 1-587, 'PRV' <DON>

A:Molecule type: DNA

A:Residues: 1-587, 'PRV' <DON>

A:Molecule type: DNA

A:Residues: 1-587, 'PRV' <DON>

A:Molecule type: DNA

A:Residues: 1-587, 'PRV' <DON>

A:Molecule type: DNA

A:Residues: 1-587, 'PRV' <DON>

A:Molecule type: DNA

A:Residues: 1-587, 'PRV' <DON>

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A:Molecule type: DNA

A:Residues: 1-587, 'PRV' <DON>

A:Molecule type: DNA

A:Residues: 1-587, 'PRV' <DON>

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 DB ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 415 PDYFINNISGVEVLVRENEEDRLRPLHYNEIRNIESPSGPGELRAYVSVHNRKKNIVAYH 468
 QY 478 ENGTMHLAPEDYGTFTSPHATQVNNQTRFISEKFGQDGLRPFQSTNTTARYTLNG 537
 DB ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 469 ENGTMHLAPEDYGTFTSPHATQVNNQTRFISEKFGQDGLRPFQSTNTTARYTLNG 528
 QY 538 NGNSYMLYLRVSSLSGNSITRTVINGRVTASVNTTNNQVNDGAFDLDINNGVNVAS 597
 DB ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 529 NGNSYMLYLRVSSLSGNSITRTVINGRVTASVNTTNNQVNDGAFDLDINNGVNVAS 587
 QY 598 DNTNVPDLINTFNSGTQFELNIMVFPNLPY 632
 DB ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 588 ANTNVPDLINTFNSGTQFELNIMVFPNLPY 622

RESULT 4

A43647
 paraoporal crystal protein cryIIAa1 - Bacillus thuringiensis subsp. israelensis
 C:Species: Bacillus thuringiensis subsp. israelensis
 C:Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 01-Dec-2000
 C:Accession: A43647; MUID:89008093; PMID:2902069
 R:Donovan, W.P.; Dankoosik, C.; Gilbert, M.P.
 J: Bacteriol. 170, 4732-4738, 1988
 A:Title: Molecular characterization of a gene encoding a 72-kilodalton mosquito-toxic crystal protein from *Bacillus thuringiensis* subsp. *israelensis*
 A:Reference number: A43647; MUID:89008093; PMID:2902069
 A:Accession: A43647
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-643 <DON>
 A:Cross-references: GB:M11737; NID:g142762; PIDN:AAA22352.1; PID:g142763
 J:Adams, L.F.; Viskic, J.E.; Whiteley, H.R.
 J: Bacteriol. 171, 521-530, 1989
 A:Title: A 20-kilodalton protein is required for efficient production of the Bacillus thuringiensis serotype 1993
 A:Reference number: A12256; MUID:89123065; PMID:2644205
 A:Accession: A12256
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 566-643 <ADA>
 A:Cross-references: EMBL:M22860; NID:g143223; PIDN:AAA22611.1; PID:g143224
 C:Genetics:
 A:Gene: cryD

Query Match 10.2%; Score 336.5; DB 2; Length 643;
 Best Local Similarity 23.1%; Pred. No. 4.5e-15;
 Matches 167; Conservative 98; Mismatches 257; Indels 201; Gaps 34;

QY 27 EHKSLDITRKEMEMKRTDHSLY-----VAP--YGVVSSFLKVKVSLIGKRIIIE 76
 DB ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 2 EHKSLDITRKEMEMKRTDHSLY-----VAP--YGVVSSFLKVKVSLIGKRIIIE 57
 QY 77 LMGILFPGSGTNLMQDILRETEOFANRLNTDLARVNAELGQANIREFNOQVNDL 135
 DB ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 58 LMGILFPGSGTNLMQDILRETEOFANRLNTDLARVNAELGQANIREFNOQVNDL 113
 QY 114 QPGFTPA-----TAKGFPLNLGSAIIQRLPGEVQYTEGVSIALFPOCTHHTL 164
 DB ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 189 RDVVLNADWEGISAATLRTYQVLYKNYTESYNYCINTYQAF--RGILNRLHDMLEPPTY 247
 DB ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 165 KDGIILASAWGFQADVDVSFLKFNQKVDYRTRLMRYVTEBEFLCKVSLDGLTFPDM 224
 QY 248 MFLNVEFYVSIWGLFPGYQSLVSSGANTLYASGSGPOQOSTSDWPFYLSLPQVNSY 305
 DB ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 225 CNLYVFPFPAANSIMKREGLKQSSLSL-----MDYGVASIPVNVNEM 267
 QY 306 -----YVANGSGARITGTFPNTIGLPGITTHALLAARVNSG-----GVSSGDITGVF 355
 DB ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 268 GGLVYKLLMGVEVNOELTIVKENV-----SFTNEPADIPARENIRGVHPTDPSGSLTGWIG 323

QY 356 N---QNFSCSTFELPPLITFPVNSMLDSGDRGNTVTWQ----- 393
 DB ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 324 NGRNTNNEFAD-----NNGNEIMEVRIQTYQVNPNNEDIAPDIINOILTA 369
 QY 394 -----TESFESTL---GLRCGAFARGN-----SNY--FPDYFIRNI 425
 DB ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 370 PAPADLFPKANADINVFQWFGSTLYGWNKIKQTYVLSNRGTIPPNYLAAGYITRI 429
 QY 426 SGVPLVYR---NEDLARPLHYNEIRNIESPSG-----TGGELRAYVSVHNRKKNIVAYH 475
 DB ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 430 SACFPGVSLAYNHDL--TTLFTNRI--EYDSPTENIIIGFADPNKDF---YKKS--- 479
 QY 476 VHENGTMHLAPEDYGTFTSPHATQVNNQTRFISEKFGQDGLRPFQSTNTTARYTLNG 532
 DB ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 480 -----HYLSETNDSYVIFPALQFAEVS--RSFLEDPPOADSDSKARFTISNEAK 529
 QY 533 YTLRNGNSYMLYLRVSSLSGNSITRTVINGRVTASVNTTNNQVNDGAFDLDINNGVNVAS 592
 DB ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 530 YSIRLN--TGFNTATRYKLI-----IKRVVPYRL--PAGIRVOSQNSGNN---RMLGSFTTA 578
 QY 593 NV-----VASDNTNVPDLINTV--TFNSGTQFELNIMVFPNLPY 632
 DB ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 579 NANEWVDFVTDAFTENDIGITTSITNALFSSISDSLSNGSEWYLSQFLVYESAFTTQI 638
 QY 629 PPI 631
 DB ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 639 NPL 641

RESULT 5

139815
 insecticidal protein cryV - Bacillus thuringiensis
 C:Species: Bacillus thuringiensis
 C:Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 26-Aug-1999
 C:Accession: 139815
 R:Gleave, A.P.; Williams, R.; Hedges, R.J.
 J:Appl. Environ. Microbiol. 59, 1683-1687, 1993
 A:Title: Screening by polymerase chain reaction of Bacillus thuringiensis serotypes for leucine subsp. kurstaki.
 A:Reference number: 139815; MUID:93298009; PMID:8517758
 A:Accession: 139815
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-719 <PES>
 A:Cross-references: GB:M98544; NID:g142767; PIDN:AAA22354.1; PID:g142768
 C:Genetics:
 A:Gene: cryV
 C:Superfamily: paraoporal crystal protein

Query Match 9.9%; Score 327.5; DB 2; Length 719;
 Best Local Similarity 22.8%; Pred. No. 2.2e-14;
 Matches 162; Conservative 103; Mismatches 271; Indels 173; Gaps 32;

QY 21 HDPSPFEHK-----SLDITRKEM--MEWKRTD-----SLY--VAP----- 52
 DB ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 9 HDPSPFNATVDKISTDSIKNETDIEIIONINHDCKKSEVENEPVSASTIQTGIGIAG 68
 QY 53 -YGVVSSFLKVKVSLIGKRIIIE LMGILFPGSGTNLMQDILRETEOFANRLNTDTTLA 111
 DB ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 69 KILGTIGVFPAGVAVSLY--SFLIGELM-----PKGR--NOMEIPEHVEEILNOKISTYARN 122
 QY 112 RVNAELGQANIREFNOQVNDLANTONPVPLSIT--SSVNTMOQLFLNRLPQRFVQYQ 170
 DB ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 123 KALTDLKGIGDALVYHDSLSVSGVGRNNTARSVVSVQYIALELMFPQKLPFAVSGEE 182
 QY 171 LLLPLPFAQANMHLSPTRDVVLNADWEGISAATLRTYQVLYKNYTESYNYCINTYQAF 230
 DB ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 183 VPLLPFYAQAANLHLRLDASIFKENGSSSEISFTNRQVBAAGYSCHCKWYKSTG 242
 QY 231 FREL--NTRILHDML---EFRTYFNLVVEFYVSIWGLFPGYQSLVSSGANTLYASGSGP 282
 DB ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 243 LNNLRGTAESVNRVNOQFRDMDLNLVALFSPSYDTQWYPIKTQAOLTRVYVTTAIGT 302

QY 283 QOQT-SFTSDM-----PFL-----YSLFOVNSN-VYLVNGESG 313
 DB 303 VHPHPSFTSTWYNNANAFSAIEAAVVRNPHLDPLEQVITYSLSRMSNTQYMMWG 362
 QY 314 ARLTQFPNIGLPGTTTHALLAARVNSGVSSGSDIGAVFNQNSCSTPLPLLPV 373
 DB 363 HXL--EERTIGGLNIST-----QGSTVTSINPVTLPFT 394
 QY 374 RSMWDSGSDRGVNTV-----NMQ--TESFESTGLRCGAFARGNSNTPD 419
 DB 395 SRDYRTESLAGNLELTPQVNGVRVDHFHKVTHPIAS-----DNFYFG 441
 QY 420 YFIRNISGVPLVVRNEDLRRLHYNEIRNIESPGTGLAAVNSVHRKNKIYA-VHE 478
 DB 442 Y-----AGIGTQLODSENELEPPAATQGPVYSYHRSHIG--LISASHVKAIVSWTHR 494
 QY 479 NGTMHLAPEDYTGFTISPIHATQV-----NNQTRTFISKEFG--NOGDSLRFGSNTTA 531
 DB 495 SA-----DRTN-TIEPNSITQIPLVKAFNLSSGAAVVRGPGTGDILR--RTNVTG 543
 QY 532 RYTLRGNGN-----SYNLYRVSSLGNSITRTINGRYVYASNVNTTNDGVNDGARF 586
 DB 544 FGDIRVNIPEPQRYRVRIRYASTTDLOPHYSINGKAINQGNFSAIMNR-----GED 596
 QY 587 LDINMGVVASDNTNVPDLINVT-----FNSGTQFELNIMFVPTNL 628
 DB 597 LDYKTFRTVGTTPPSFLDQSTFTIGAMNFSGNEVYIDRIEFVPEV 645

RESULT 6

S25383
 Parasporal crystal protein cryIIA - *Bacillus thuringiensis*
 N/A:Accession: delta-endotoxin, parasporal crystal protein cryV
 C/Species: *Bacillus thuringiensis*
 C/Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 01-Dec-2000
 C/Accession: S25383
 R/Factor: R.; Tipset: J.; Gibb, G.; Pells, S.; Pike, D.; Jordan, L.; Ely, S.
 Mol. Microbiol. 6, 1211-1217, 1992
 A>Title: Identification and characterization of a novel *Bacillus thuringiensis* delta-end
 A/Reference number: S25383; MUID:92265582; PMID:1588820
 A/Accession: S25383
 A/Molecule type: DNA
 A/Residues: 1-719 <ID>
 A/Cross-references: EMBL:X62821; NID:940289; PIDD:CAA44633.1; PID:940290
 C/Genetics:
 A/Gene: cryV
 C/Superfamily: parasporal crystal protein
 C/Keywords: delta-endotoxin

Query Match 9.8%; Score 324.5; DB 2; Length 719;
 Best Local Similarity 22.8%; Pred. NO. 3.5e-14;
 Matches 162; Conservative 102; Mismatches 272; Indels 173; Gaps 32;
 QY 21 HDPSFEHK-----SLDTRIKEM-MEMKRTDH-----SLY--VAP----- 52
 DB 9 HQSSSNKAVDKISTDSLKNETDIELQNIHNEBCLKMSEYENVEFPVASITQIGIGAG 68
 QY 53 -IVGVSSFLKKVSGSLGKRLSELKGLIFPGSGTNLMODILRETFQFNOLNTDTLA 111
 DB 69 KILGLGVPPAGVAVSLY-SFLIGELM-----PKGK-NQMEIFMEHVEITINQKISTYARN 122
 QY 112 RVNAELBGLQANIREFNOQVNFNPTQNPVPLSIT--SSVNTMOQLFLNRLPQFVQYQ 170
 DB 123 KALTDLKGDLALAVYHDSLESVNGNRNNTFARVSVGYIALEIMFVOKLPSFVSGEE 182
 QY 171 LLLPLPAQANMELSFTRDVVLANDEMGISAATLRYQNYLAKYTTESYNYCINTYOTA 230
 DB 183 VPLLPITYAQANLHLHLLDASIFGKEWGLSSSEISFTFIRQVBERAGDYHCVKWTSG 242
 QY 231 FRGL-NTRLHDMU---EFFTYMFLNVEFVYSIMSLFKYQSLVSSGANL-----YASGSGP 282
 DB 243 LNNLRGTNLESVVRNQFRDMDTLNVLVALPSPYDTQWYPIKTTAQLTRVYTDALGT 302

QY 283 QOQT-SFTSDM-----PFL-----YSLFOVNSN-VYLVNGESG 313
 DB 303 VHPHPSFTSTWYNNANAFSAIEAAVVRNPHLDPLEQVITYSLSRMSNTQYMMWG 362
 QY 314 ARLTQFPNIGLPGTTTHALLAARVNSGVSSGSDIGAVFNQNSCSTPLPLLPV 373
 DB 363 HXL--EERTIGGLNIST-----QGSTVTSINPVTLPFT 394
 QY 374 RSMWDSGSDRGVNTV-----NMQ--TESFESTGLRCGAFARGNSNTPD 419
 DB 395 SRDYRTESLAGNLELTPQVNGVRVDHFHKVTHPIAS-----DNFYFG 441
 QY 420 YFIRNISGVPLVVRNEDLRRLHYNEIRNIESPGTGLAAVNSVHRKNKIYA-VHE 478
 DB 442 Y-----AGIGTQLODSENELEPPAATQGPVYSYHRSHIG--LISASHVKAIVSWTHR 494
 QY 479 NGTMHLAPEDYTGFTISPIHATQV-----NNQTRTFISKEFG--NOGDSLRFGSNTTA 531
 DB 495 SA-----DRTN-TIEPNSITQIPLVKAFNLSSGAAVVRGPGTGDILR--RTNVTG 543
 QY 532 RYTLRGNGN-----SYNLYRVSSLGNSITRTINGRYVYASNVNTTNDGVNDGARF 586
 DB 544 FGDIRVNIPEPQRYRVRIRYASTTDLOPHYSINGKAINQGNFSAIMNR-----GED 596
 QY 587 LDINMGVVASDNTNVPDLINVT-----FNSGTQFELNIMFVPTNL 628
 DB 597 LDYKTFRTVGTTPPSFLDQSTFTIGAMNFSGNEVYIDRIEFVPEV 645

RESULT 7

139814
 Insecticidal protein cryVI - *Bacillus thuringiensis*
 C/Species: *Bacillus thuringiensis*
 C/Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 26-Aug-1999
 C/Accession: 139814
 R/Shin, B.S.; Park, S.H.; Choi, S.K.; Koo, B.T.; Lee, S.T.; Kim, J.I.
 Appl. Environ. Microbiol. 62, 2402-2407, 1995
 A>Title: Distribution of cryV-type insecticidal protein genes in *Bacillus thuringiensis*
 A/Reference number: 139814; MUID:95314293; PMID:7793960
 A/Accession: 139814
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-719 <RES>
 A/Cross-references: GB:L6338; NID:9540281; PIDD:AAC36999.1; PID:9540282
 C/Genetics:
 A/Gene: cryVI
 C/Superfamily: parasporal crystal protein

Query Match 9.8%; Score 324.5; DB 2; Length 719;
 Best Local Similarity 22.8%; Pred. NO. 3.5e-14;
 Matches 162; Conservative 102; Mismatches 272; Indels 173; Gaps 32;
 QY 21 HDPSFEHK-----SLDTRIKEM-MEMKRTDH-----SLY--VAP----- 52
 DB 9 HQSSSNKAVDKISTDSLKNETDIELQNIHNEBCLKMSEYENVEFPVASITQIGIGAG 68
 QY 53 -IVGVSSFLKKVSGSLGKRLSELKGLIFPGSGTNLMODILRETFQFNOLNTDTLA 111
 DB 69 KILGLGVPPAGVAVSLY-SFLIGELM-----PKGK-NQMEIFMEHVEITINQKISTYARN 122
 QY 112 RVNAELBGLQANIREFNOQVNFNPTQNPVPLSIT--SSVNTMOQLFLNRLPQFVQYQ 170
 DB 123 KALTDLKGDLALAVYHDSLESVNGNRNNTFARVSVGYIALEIMFVOKLPSFVSGEE 182
 QY 171 LLLPLPAQANMELSFTRDVVLANDEMGISAATLRYQNYLAKYTTESYNYCINTYOTA 230
 DB 183 VPLLPITYAQANLHLHLLDASIFGKEWGLSSSEISFTFIRQVBERAGDYHCVKWTSG 242
 QY 231 FRGL-NTRLHDMU---EFFTYMFLNVEFVYSIMSLFKYQSLVSSGANL-----YASGSGP 282
 DB 243 LNNLRGTNLESVVRNQFRDMDTLNVLVALPSPYDTQWYPIKTTAQLTRVYTDALGT 302

QY 283 CQTD-SFTSQDW-----PFL-----YSLFQVNSN-YVINGPSG 313
 DB 303 VHPSPSTSTWYNNNAPSFSAIEAAVVRNPHLDLFLEQVYISLISRMSTNQVMNMG 362
 QY 314 ARLTQFPNIGLPGTTTHALLAAVNVSGSGDIGNVNONSCSTFLPULFPV 373
 DB 363 HKL--BFTIGGTANIST-----QGSTNTSINPVLPT 394
 QY 374 RSWLSDSGDRGVNTVT-----NMQ--TESHSTLGRCAFTARGNSNPPD 419
 DB 395 SRDYRTESLAGNLFLOPVNGVPRVDHMFVTHPLAS-----DNFYPG 441
 QY 420 YFRNISGVLVVRNEDLRPLHNYEIRIESPGTGGRAVMSYNNRKNITYA-VHE 478
 DB 442 Y-----AGIGTQLODSENEPFPRAQCPYTESYSHRSHIG--LTSASHVAVLSWTR 494
 QY 479 NGMTHLABEDYGTFTSPHATOV-----NNOGRTFISEKFG--NOGDSLRFEOSNTYA 531
 DB 495 SA-----DRTN--TTEPNSITQIDPVKAFPLSSGAAVRGFGTGDILR--RTVGT 543
 QY 532 RYLRGNNGN-----SYMLYLRVSSLSGNSTIRVTNGRVYTAASVNTTNNNGVNDGARF 586
 DB 544 FGDIVNINPPAQRVVRKRYASTDLOFTHSINGKAINQGNFSATMR-----GED 596
 QY 587 LDINMGVYASDNTNVPLDINTV-----FNSGTQFELMNIMFVPTNL 628
 DB 597 LDYKTFRTVGTTPFSFLDVOSTFTIGAMNFSQNEVYIDRIEFVPEV 645

RESULT 8

140590

CRYV465 protein - *Bacillus thuringiensis*C.Species: *Bacillus thuringiensis*

C.Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 26-Aug-1999

C.Accession: I40590

R.Shin, B.S.; Park, S.H.; Choi, S.K.; Koo, B.T.; Lee, S.T.; Kim, J.I.

Appl. Environ. Microbiol. 61, 2402-2407, 1995

A>Title: Distribution of cryV-type insecticidal protein genes in *Bacillus thuringiensis* tomocidus.

A.Reference number: 139814; MUID:95314293; PMID:7793360

A.Accession: I40590

A.Status: preliminary; translated from GB/EMBL/DBJ

A.Molecule type: DNA

A.Residues: 1-719 <RES>

A.Cross-references: EMBL:U07642; NID:g467234; PIDD:AAA82114.1; PID:g467235

C.Genetics:

A:Gene: cryV465

C:Superfamily: parasporal crystal protein

Query Match 9.4%; Score 310.5; DB 2; Length 719;
 Best Local Similarity 22.7%; Pred. No. 3.1e-13;
 Matches 153; Conservative 116; Mismatches 259; Indels 145; Gaps 34;

QY 27 EHKSLDTRKEMWKRTHSLYVA-PIYGVSSFLKKVGLSGKRISELWGLFPG 85
 DB 47 EHSID-----PVSASITQIGIGKIGLIGTPPAGQIASLY-SLISELM---PKG 97
 QY 86 STNLMQDLRTGQFLNQLNTDTLAVNAELSGLANIREFNOQVNFNPTQNEVPLS 145
 DB 98 KQO-WELFMEHVEIINOKILTYANRKLSPDLGDLALAVYHESLWVENNNTARRS 156
 QY 146 IT-SSEVNTMOQLFLNLPORVQYQOLLPLFPAQANWELSPFRLVLAADWIGSAT 204
 DB 157 VVKNGYALBELMFQGLPSFANSGEVLPIPIYAQANHLHLRLDSDIGKWKGLSASE 216
 QY 205 LATTQNYKATYTESNYCINTYOTA--FRGLNTELDML-ERTTWMPLNVEVYSIMS 260
 DB 217 ISTFNKQVETRDYSDHCICKYNTGNLNLKGNNAKSWVRVQPRKMTMLMVLVLP 276
 QY 261 LEKQSL--VSSGANL-----YASGSGP--QOTQSFQSWPPLSLPQVSNVNLGSG 313
 DB 277 --SYDLTVYPIKTTSQLTREVVTAIGVHPNQAFASTW-----YNNAPSPSAIE 326

QY 314 ARLTQFPNIGLPGTTTHALLA-----ARVNSGG--VSSGDIQAVNONSCSTFLP 366
 DB 327 AAVIS- PHLDLFLEKTYISLISRMSTNQVMNMGHRLSERPGALNT----- 376
 QY 367 PLTPFPVSWLSDSGDRGVNTVMQTESP-----ESTLGRCAFTARGNSNPP 418
 DB 377 -----STQGSTNTSINPVLQFTSRDYRTESLAGNL----- 409
 QY 419 DYFRNISGV-----LVNNEDLRPLHNYEIRIESPGTGGRAVMSYNNRKNITYA-VHE 457
 DB 440 -FLTPVNGVVRNEDLRPLHNYEIRIESPGTGGRAVMSYNNRKNITYA-VHE 478
 QY 458 GLRAY-----WVSVNKRKNITYA-VHNGTMHLABEDYGTFTSPHATOV----- 503
 DB 465 NYESYSHRSHIGLISASHVKALVYSWTHRSA-----DRTN--TTEPNSITQIDPVKA 515
 QY 504 -NNOGRTFISEKFG--NOGDSLRFEOSNTYARLYRGNNGN-----SYMLYLRVSSLSGNST 556
 DB 516 FULSSGAAVRGFGTGDILR--RTVGTFGDIVNINPPAQRVVRKRYASTDLOF 573
 QY 557 RYLRGNNGN-----SYMLYLRVSSLSGNSTIRVTNGRVYTAASVNTTNNNGVNDGARF 586
 DB 574 HTSINGKAINQGNFSATMR--GEDLDYKTFRTVGTTPFSFLDVOSTFTIGAMNFSQNE 632
 QY 616 FELMNIMFVPTNL 628
 DB 633 VVIDRIEFVPEV 645

RESULT 9

S49247

parasporal crystal protein cryCa1 (validated) - *Bacillus thuringiensis*

N.Alternate names: parasporal crystal protein cryJH

C.Species: *Bacillus thuringiensis*

C.Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 01-Dec-2000

R.Lambert, B.; Bussse, U.; Decock, C.; Jensen, S.; Pien, C.; Saey, B.; Seurinck, J.; V

Appl. Environ. Microbiol. 62, 80-86, 1996

A>Title: A *Bacillus thuringiensis* insecticidal crystal protein with a high activity agai

A.Reference number: A59350; MUID:96141404; PMID:8572715

A.Accession: A59350

A.Molecule type: DNA

A.Residues: 1-1157 <LAM>

A.Cross-references: EMBL:Z37527; NID:9547554; PIDD:CAA85764.1; PID:9547556

A.Experimental source: serovar colworth

C:Comment: This parasporal crystal protein, active against corn borer and other insects,

C:Superfamily: parasporal crystal protein

Query Match 9.3%; Score 307; DB 1; Length 1157;
 Best Local Similarity 23.4%; Pred. No. 1.1e-12;
 Matches 163; Conservative 87; Mismatches 215; Indels 232; Gaps 34;

QY 52 PIYGVSSFLKKVGLSGKRISELWGLFPGSTNLMQDLRTGQFLNQLNTDTL 111
 DB 87 PFSQIVSFY-----QFLANTLM-----PVNDTALWEAFNRQVEELVNOQITEPARN 133
 QY 112 RVNAELSGLANIREFNOQVNFPL--NPTQNPVPLSTSSVNTMOQL-FLNRLPQRYQ 167
 DB 134 QALRLQSGDGFNNYQSGLSLQNLMLABNDTR--LSVRAQPLADLPVNAIPLEFVN 190
 QY 168 GYQLLLPLFPAQANWELSPFRLVLAADWIGSATLRTYQNYLKNYTESNYCINTY 227
 DB 191 GQVPLISVYAQVNLHLKDLKASLFGGWMGFTGSEISTYVROLELFAKYVWCETWY 250
 QY 228 QTA--FRGLNTELDML-ERTTWMPLNVEVYSIMS 260
 DB 251 NTGDLRLKGNTHESLRYH--QFRKEMTVLVLDV--ALFFYDY-----RLIFPGS 298
 QY 261 GPQQTQS-FTS-----QVM-----PFLY-----S 298
 DB 299 NPQLTREVTYDPIVNPANVGLCRMGTPNPTNTFSELENAPIRPPLHLDLNSLTYSN 358

QY 299 LFOVNSNYVINGSGARLTOTFPNIGLPG-----TTTTALLAARVNSGVSSEDIG- 352
 DB 359 RFPVSSNF-MDYMSHTLRSLYNDSDAVQDSYGLITTTATINPEVGTNRISITANDP 417
 QY 353 -----AVFNQNSCSTFLPPLTPFVRSWLDGSD--RCGVNTV--TNMOTESFESTUG 402
 DB 418 RSLMIGIYGVN-----RASFPVGLFNGTITSPANGCGCDLVDNDELPEDEST-- 465
 QY 403 LRCAFTPAAGSNVPEPY-----FRNISGYPVLY--RNEQRLRPLHNEINISBP 453
 DB 466 ---GSSHTRLSHVTFFSQTNQAGSIANAGSPYVWTRDVDNNTTIPKRIQLP-- 519
 QY 454 GTFQGLRAYVSVNHRKNITVAVHNGTMIHLAPEDYGTFTSPHATOVNNQTRTEISE 513
 DB 520 -----LVKA-----SAPVSGTIVLGP-----GFT----- 539
 QY 514 KFGNQDGLRFGQSTTARTYTLKGNNS-----YULYIRVSLGNSGTIRVTIN---GRV 564
 DB 540 ---GGGILIRTTNGTFG--TLRYVNSPLTQOYHLRVRPASTGANSILVLRGVSIGDY 593
 QY 565 YTSANVY-----TTT-----NNDGVNDGAPFLD-- 588
 DB 594 RLGSITWNRQGLTYESFTRFTTGPFPFTQAOELITVNAEGVSTGGEYIIDRIE 653
 QY 589 ---INMGVNVASD-----NTNVPIDIVNT 609
 DB 654 IVPNPARAEEDLEAKKAVASLFTRTDGLQVNT 690

RESULT 10

A48970
 parasporal crystal protein cryICB - *Bacillus thuringiensis*
 C/Species: *Bacillus thuringiensis*
 C/Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 01-Dec-2000
 R/Kalman, S.; Kienne, K.L.; Libs, J.L.; Yamamoto, T.
 Appl. Environ. Microbiol. 59, 1131-1137, 1993
 A/Title: Cloning of a novel cryIC-type gene from a strain of *Bacillus thuringiensis* subsp.
 A/Reference number: A48970; NCBI:93236401; PMID:8476286
 A/Accession: A48970
 A/Status: preliminary
 A/Molecule type: nucleic acid
 A/Residues: 1-1176 <KAL>
 A/Sequence: GB:W97880, NID:9289263
 A/Experimental source: subsp. galleriae HD29
 A/Note: sequence extracted from NCBI backbone (NCBIN:129672, NCBI:129675)
 C/Superfamily: parasporal crystal protein
 C/Keywords: delta-endotoxin

Query Match 8.9%; Score 294.5; DB 2; Length 1176;
 Best Local Similarity 22.6%; Pred. No. 7,9e-12;
 Matches 160; Conservative 110; Mismatches 246; Indels 191; Gaps 38;
 QY 2 NVNINNGRTTICAVYVVAH-----DPFSEHKSLDTTRKEMEMKRTDHSIYAPI 53
 DB 3 NNINQNC-----CVPYNCISNPEKILLDERISITGNSIDI-----SISVLQ 44
 QY 54 VCTVSSFLKKGSLIGKRLISELWGLIPPSGSTNLMODILRETEQFLNORLNTDTLAV 113
 DB 45 L--VSNF-VFEGGFLVG--LDFVWGLVGP--WDALVQIEQLINRIIAAARSA 95
 QY 114 NAELEGLQANIREFNOQVDFLN--PTQNPVLS-TISSVNTMOQLFNLRLPQVVOGY 169
 DB 96 ISNLEGLGN--FNIVYAEFKEWADPNPVRTRVDRRIIDGLERDIPSRILGF 152
 QY 170 QLLILPLPAQANMHLSPTRDVVLANDEWGISATLTQYVLYKNTYTESNYCINTYQT 229
 DB 153 EYPLISVYQAANMHLAILRDSIFGARGKLTINNENYMLRIHIDEVAHACADTN- 211
 QY 230 AFRGLN---TRLHMLER---RTYMLANFEVYSIWSLFFKQSLVSSGANL-----YAS 278
 DB 212 --RGLNLPKSTYQDWITYNRLRDLTLVLDIAAFPSYDNRRTPIQSVGLTREITYD 269

QY 279 ---GSGPQ-----QTSFTSDP-----WPLYSL-----FOVNSNYVINGSGAR 315
 DB 270 PLITNRPQLQSVNQLTFFVNMESNAIRTPHLFDVNLNLTIFDMFVSGRFVWG-- 324
 QY 316 LVQTPNIGLPGTTTTALLAARVNSGVSAGDI GAVFNO--NFSGS-----TFLP 366
 DB 325 -----HVISNRIG-GGNITSPYIGRANQEPBSFTTNGVVRITLSN 366
 QY 367 PLITFVRSWLDGSDRGCVNTVNMOTESFESTUGLRGAFARGNSNPEPYIRNIS 426
 DB 367 PFRRLQPPWAPPPFLRGVEV-----EFSTPL-----NSFTYRGHGT-----VDSIT 410
 QY 427 GVP-----LVKREDRLRPLHNEINISBPSTPGCLAYVSVNHRKNITV--AVHE- 478
 DB 411 ELPPEDNSVPRRGYSHRLCHATFVQSGTFLTPGVSHTWSAIDRIIITPDYINQI 470
 QY 479 -----NGTMIHLAPEDYGTFTSPHATOVNNQTRTEISEKFNQDGLRFGQST 529
 DB 471 PLVKAFLNLTSGTSVVGPF--GFTGDIIRTVNNGSVLSM-----SLNF--SNT 514
 QY 530 TARTYLRGNGSNYULYIRVSLGNSGTIRVTINGRVYTAANVTTTNDG--VNDNGA- 584
 DB 515 TLQ-----RIRVRKYASQTMWSVYVG-----STTGNGQFPSTMSANGL 557
 QY 585 -----RFLDIMGVNVASDNTNVPIDIVTENSQTQ-FELANINFEV 625
 DB 558 TSGSFRALEFPVG-ISASGQGA--SISISNNVGRQMFHLDIRIEFLP 601

RESULT 11

JT0241
 parasporal crystal protein - *Bacillus thuringiensis* (strain aizawai IPL7)
 N/Alternate names: 135k insecticidal protein
 C/Species: *Bacillus thuringiensis*
 C/Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 01-Dec-2000
 R/Shimizu, M.; Oshie, K.; Nakamura, K.; Takada, Y.; Oeda, K.; Ohkawa, H.
 Agric. Biol. Chem. 52, 1565-1573, 1988
 A/Title: Cloning and expression in *Escherichia coli* of the 135-kDa insecticidal protein
 A/Reference number: JT0241
 A/Accession: JT0241
 A/Molecule type: DNA
 A/Residues: 1-1176 <SHI>
 A/Note: b. thuringiensis aizawai IPL7 produces similar 130K and 135K insecticidal proteins
 C/Comment: The 135K protein has insecticidal activity against *Plutella xylostella* larvae
 C/Superfamily: parasporal crystal protein
 C/Keywords: delta-endotoxin

Query Match 8.5%; Score 282.5; DB 2; Length 1176;
 Best Local Similarity 21.7%; Pred. No. 5.2e-11;
 Matches 152; Conservative 105; Mismatches 271; Indels 173; Gaps 29;
 QY 6 NNGRTTICAVYVVAHDPFSEHKSLDTTRKEMEMKRT--DHSIYAPIGVTSFLIK 63
 DB 3 NNININCEIPNCS-----NPEVVLGGERIEGTYPIDISL-----SLTGELS 48
 QY 64 K-----VGSILGRILISELWGLIPPSGSTNLMODILRETEQFLNORLNTDTLAV 119
 DB 49 EYVAGAGFLG--LVDIITWIGFSPS-----QMDALVQIEQLINRIIEFARNQISLIS 102
 QY 120 IQ-----ANIREFNOQVDFLNPTQNPVLSITSSVNTMOQLFNLRLPQVVOGY 172
 DB 103 LSNLYQIVAESFREME-----ADPTNPLRBEKRIQFNDMSALTTAIPFAVQVQVP 156
 QY 173 LPLPLFOAANMHLSPTRDVVLANDEWGISATLTQYVLYKNTYTESNYCINTYQAF 232
 DB 157 LLSVYQAANMHLSTLSDVSVFGQRGVPAATNSRYNDLTLLIGNYTDVAVRYNTGLE 216
 QY 223 ---GLNTRLHMLER---EFRTYMLANFEVYSIWSLFFKQSLVSSGANL--YASGSGPQQTQ 286
 DB 217 RYWGPPSR--DWVRNQGFRRELTLVLDIIVLFS-----NYDSRRYPIRTY 260
 QY 287 SFTSQDWPLVLSLFOVNSNYVINGSGA-----RLQTP--PNIGGLPGTTTTALLAA 338

[illegible]

Db 361 GGRRL--EFFRTIGMLNTST 378

RESULT 14

paraaporal crystal protein cryAel - *Bacillus thuringiensis* (strain aleeti)
A:Accession: A41052
C:Species: *Bacillus thuringiensis*
C>Date: 03-Apr-1992 #sequence_revision 03-Apr-1992 #text_change 01-Dec-2000
C/Accession: A41052
R:Lee, C.S.; Aronson, A.I.
J. Bacteriol. 173, 6635-6638, 1991
A:Title: Cloning and analysis of delta-endotoxin genes from *Bacillus thuringiensis* subsp.
A:Reference number: A41052; MUID:92011442; PMID:1655719
A:Accession: A41052
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1181 <LEB>
A:Cross-references: GB:W65252; NID:q142874; PIDN:AAA22410.1; PID:q142875
C:Superfamily: paraaporal crystal protein
C:Keywords: delta-endotoxin

Query Match 8.4%; Score 277; DB 2; Length 1181;

Best Local Similarity 22.3%; Pred. No. 1.2e-10;

Matches 159; Conservative 106; Mismatches 252; Indels 196; Gaps 33;

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Qy 6 NNGRTTICAYNVVAHDPEFSEHKSIDTIRKEMWERT--DHSLYAPVIGTVSSFLIK 63
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3 NNPKNICEIPYNCLIS-----NPEVVLGGERIETGYTPIDISL-----SLTQFLIS 48
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 64 K---VSLIGKRIILSELWGLIPSGSTNMQDILRETOFNLQRLNTDLARVALELG 119
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 49 EYPVGAAPVLG--LIDLIMGFVPS---QMDAFVLQIEQLISQRIEFARNOALSRLG 102
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 120 LOANI-----RENOOVNPLNPNQVPLSTSSVNTMOQLFNLPLQFVQYQL 171
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 103 L-SNLQIYAEAFRE-----ADPTNPALEEMRIQFNDMSALTTAIPLAOVNVP 155
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 172 LILPLFAQANMELSTIRDVVLNADENGISAATLRTYQNYLKNYTEYSNYCINTYQAF 231
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 156 PLISVYQAVNLHLSTLRDVSFGQWGLDVALTINRNVNLTIRLIGYTDYAAVRYNGL 215
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 232 R---GLNTRLHDML---EFFRTMPLNFEVYSIWSLFFKQSLVSSGANLVYSGSGPOQT 285
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 216 ERWGPDSR--DWVRNQFRRELTLTVLDIVLSLP-----NYDSRYPIRT 259
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 286 QSFSDWPEPLYSLPQVNSNYVLNGFSGA-----RLYQTF--PNIGLPGTTT-- 332
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 260 VSQLR-----EITYNPVLENFDSFRGSAQRIEQSIRSPHLMIDINSITYTDAH 310
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 333 -----HALLAARNVSGVSS-----GDIQAVFNO-----NFGSTPLPPL 368
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 311 GGYVYVSGHQIMASPVGFSGPEFTPELYGTGNAAPQNTVIAQAGQVYTTLSSTP--Y 367
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 369 LTFPVRSWLDSGDRGVNTVTNMQTESFESTLGRCAFTARGNSVFPDYFIR----- 423
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 368 RMPFI-----GIN-----NORLSVLDGTEFAYGSSNLBSAVYRKSGTV 407
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 424 -NISGVPLVYRNEDLR-----RLAYNEINISPSGTCGRLAYVSVNKR--NNIY 474
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 408 DSLDSIPPODNNVPEPQFSHRLSHVSFMSGSGNSV--SIRKAPMSWIRKAEFNII 466
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 475 AVHE-----NGTMIHLAPEDYGTFTSPHATQVNNQTRTFISEKFGQDGS 521
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 467 PSSQITQIPLFKSTNLGSGTVKGP--GFT-----GGDI 499
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 522 LTFEOSTNTAATYTRG-----GNSYNLYLRVSSLSNSTIRVTINGRYTASVNTTNN 576
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 500 LR--RTSPQGISLIRVITAPISQRYRIRIVASTNLQFTSTIDGRINQGSFATMS 557
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 577 DGVNDGARFLDINMGVVAADNTVPLDINV--TPNSGQPELMNIMEVPTNL 628
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 558 GGNLQSGS--FRTVGFTTPNFNSGSSVFTLSAHVNSGNEVYIDRIEFPVAV 609
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

RESULT 15

paraaporal crystal protein cryIAa - *Bacillus thuringiensis*
A:Accession: J02219
C:Species: *Bacillus thuringiensis*
C>Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 01-Dec-2000
C/Accession: J02219
R:Udayasuriyan, V.; Nakamura, A.; Mori, H.; Maacki, H.; Uozumi, T.
Biosci. Biotechnol. Biochem. 58, 830-835, 1994
A:Title: Cloning of a new cryIA(a) gene from *Bacillus thuringiensis* strain FU-2-7 and ar
A:Reference number: J02219; MUID:94289859; PMID:7764972
A:Accession: J02219
A:Molecule type: DNA
A:Residues: 1-1176 <UDA>
A:Cross-references: DDBJ:D17518; NID:9506190; PIDN:BA04468.1; PID:9535781
C:Genetics:
A:Gene: cryIA(a)
C:Superfamily: paraaporal crystal protein
C:Keywords: delta-endotoxin

Query Match 8.3%; Score 276.5; DB 2; Length 1176;

Best Local Similarity 21.5%; Pred. No. 1.3e-10;

Matches 151; Conservative 105; Mismatches 272; Indels 173; Gaps 29;

```

Qy 6 NNGRTTICAYNVVAHDPEFSEHKSIDTIRKEMWERT--DHSLYAPVIGTVSSFLIK 63
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3 NNPKNICEIPYNCLIS-----NPEVVLGGERIETGYTPIDISL-----SLTQFLIS 48
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 64 K---VSLIGKRIILSELWGLIPSGSTNMQDILRETOFNLQRLNTDLARVALELG 119
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 49 EYPVGAAPVLG--LVDILIMGFPS---QMDAFVLQIEQLISQRIEFARNOALSRLG 102
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 120 LQ-----ANIRENOOVNPLNPNQVPLSTSSVNTMOQLFNLPLQFVQYQL 172
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 103 LSNLQIYAESPREME-----ADPTNPALEEMRIQFNDMSALTTAIPLAOVNVP 156
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 173 LILPLFAQANMELSTIRDVVLNADENGISAATLRTYQNYLKNYTEYSNYCINTYQAF 232
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 157 LLSVYQAVNLHLSTLRDVSFGQWGLDVALTINRNVNLTIRLIGYTDYAAVRYNGL 216
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 233 ---GLNTRLHDML---EFFRTMPLNFEVYSIWSLFFKQSLVSSGANLVYSGSGPOQT 286
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 217 RWGPDPSR--DWVRNQFRRELTLTVLDIVLSLP-----NYDSRYPIRT 260
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 287 SFTSDWPEPLYSLPQVNSNYVLNGFSGA-----RLYQTF--PNIGLPGTTT-- 338
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 261 SQLR-----EITYNPVLENFDSFRGSAQRIEQSIRSPHLMIDINSITYTDAH 311
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 339 RVNYSGG--VSSGDIQAVFNOFSCSTP-----LPPLLP----- 371
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 312 GNNVSGHQITASPVG-----PSGPEFAFPLFGNAGNAAPVLYSLTGLGIFFTLSPL 365
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 372 PVSWSLDSGDRGVNTVTNMQTESFESTLGRCAFTARGNSVFPDYFIRINISGPLV 431
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 366 YRRLIISGEPNOELFVLDTGERSFSLTTLNLPSTYRQGT-----VDSLDAVPP 417
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 432 VRNEDLRRLAY--NEIRNISPSGTCGRLAYVSVNKR--NNIYAVHE----- 478
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 418 DNSVPRAGFSHRLSHVYMLSOAGAVYTLRAPFVSQHSABFNIIIPSSQITQIPLTK 477
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 479 ---NGTMIHLAPEDYGTFTSPHATQVNNQTRTFISEKFGQDGSIFEGQNTTARY 533
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 478 STNLGSGTVKGP--GFT-----GGDILR--RTSPQGIS 508
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 534 TLRGN-----GNSYNLYLRVSSLSNSTIRVTINGRYTASVNTTNDGVNDGARFLD 568
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 509 TLRVNITAPISQRYRIRIVASTNLQFTSTIDGRINQGSFATMS--GSNLSGSGFRT 567
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 589 INMNVVVAADNTVPLDINV--TPNSGQPELMNIMEVPTNL 628
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 568 VGFPTTPNFNSGSSVFTLSAHVNSGNEVYIDRIEFPVAV 608
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

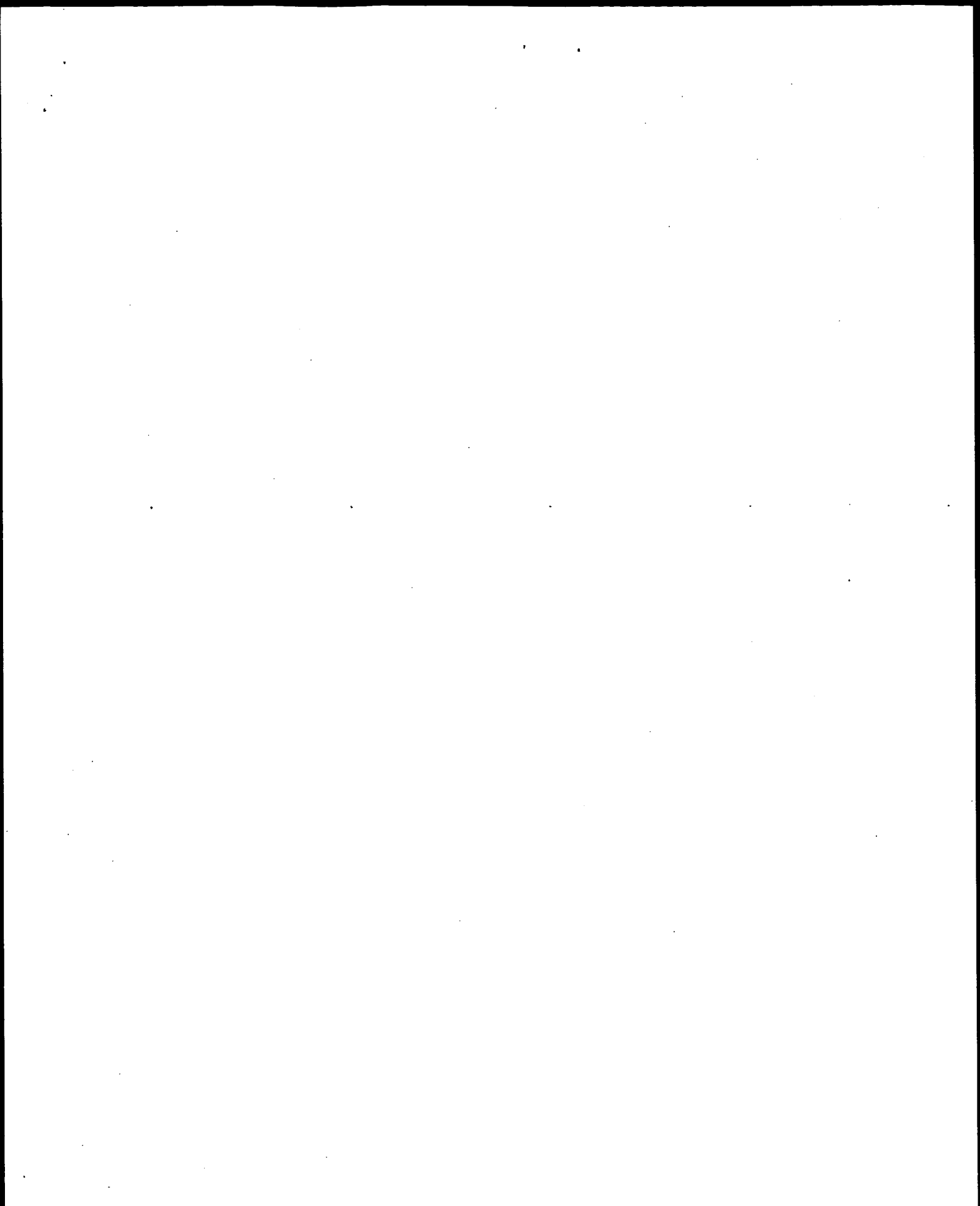
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Fri Aug 15 11:51:36 2003

us-10-040-906a-2.rpr

Page 9

Search completed: August 14, 2003, 18:12:44
Job time : 29 secs



GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 14, 2003, 18:08:22 ; Search time 15 Seconds
(without alignments)
1981.392 Million cell updates/sec

Title: US-10-040-906a-2

Perfect score: 3314
Sequence: 1 MNVVLNGRTTICDANVVA.....GTQFLNIMIPVPTNLPPIY 632

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues
Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	3048.5	92.0	633 1 C2AA_BACTK	P21253 bacillus th
2	3010.5	90.8	633 1 C2AB_BACTK	P21254 bacillus th
3	2916.5	88.0	633 1 C2AD_BACTK	O9rmg3 bacillus th
4	2545	76.8	622 1 C2AC_BACTK	O45743 bacillus th
5	1887	32.8	675 1 C1BA_PABPP	P57091 paenibacill
6	1080	32.6	706 1 C1AA_PABPP	O45358 paenibacill
7	1073.5	32.4	695 1 C1CA_PABPP	P57092 paenibacill
8	336.5	10.2	643 1 C2AA_BACTI	P21256 bacillus th
9	327.5	9.9	719 1 C1IA_BACTK	O45752 bacillus th
10	327.5	9.9	1231 1 C1BD_BACTZ	O9za25 bacillus th
11	325	9.8	719 1 C1ID_BACTU	O9xd11 bacillus th
12	310.5	9.4	719 1 C1IB_BACTE	O45709 bacillus th
13	307	9.3	1157 1 C9CA_BACTO	O45733 bacillus th
14	306	9.2	1138 1 C7AB_BACTA	O45707 bacillus th
15	303.5	9.2	1227 1 C1BE_BACTU	O85805 bacillus th
16	304.5	9.2	750 1 C8BB_BACTV	O9z1u5 bacillus th
17	300.5	9.1	682 1 C1BA_BACTH	O86170 bacillus th
18	294.5	8.9	1176 1 C1CB_BACTG	P56953 bacillus th
19	293.5	8.9	1229 1 C1BB_BACTU	O45774 bacillus th
20	293.5	8.9	1233 1 C1BC_BACTM	O45716 bacillus th
21	291.5	8.8	1179 1 C1AD_BACTA	O03744 bacillus th
22	288.5	8.7	1138 1 C7AB_BACTU	O45708 bacillus th
23	287	8.7	724 1 C8BA_BACTU	O45730 bacillus th
24	282.5	8.5	1169 1 C8BA_BACTU	O45705 bacillus th
25	280	8.4	1169 1 C9DA_BACTP	O06014 bacillus th
26	277	8.4	1181 1 C1AE_BACTL	O03740 bacillus th
27	275.5	8.3	1170 1 C1JB_BACTU	O45715 bacillus th
28	275.5	8.3	1228 1 C1BA_BACTK	P05517 bacillus th
29	273	8.2	1215 1 C1KA_BACTM	O45715 bacillus th
30	272.5	8.2	826 1 C8AA_BACTH	O98597 bacillus th
31	271.5	8.2	1176 1 C1AA_BACTK	O03745 bacillus th
32	270.5	8.2	1174 1 C1EB_BACTA	O03745 bacillus th
33	268	8.1	1155 1 C1AB_BACTK	P06578 bacillus th

34	267.5	8.1	1178 1 C1AC_BACTK	P05068 bacillus th
35	266	8.0	1167 1 C1JA_BACTU	O45738 bacillus th
36	265	8.0	1174 1 C1PA_BACTA	O03746 bacillus th
37	264.5	8.0	1160 1 C8CA_BACTP	O45706 bacillus th
38	261.5	7.9	1172 1 C1HA_BACTU	O45748 bacillus th
39	261	7.9	1169 1 C1FB_BACTM	O66377 bacillus th
40	260.5	7.9	1163 1 C0AA_BACTF	O9x597 bacillus th
41	259	7.8	1165 1 C1DA_BACTA	P19415 bacillus th
42	258.5	7.8	1176 1 C1GA_BACTU	O98515 bacillus th
43	255.5	7.7	649 1 C3CA_BACTK	O45744 bacillus th
44	253	7.6	1138 1 C7AA_BACTU	O03749 bacillus th
45	253	7.6	1150 1 C9EA_BACTA	O9znl9 bacillus th

ALIGNMENTS

RESULT 1
ID C2AA_BACTK STANDARD: PRT: 633 AA.
AC P21253; 052764;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pepticidal crystal protein cry2Aa (insecticidal delta-endotoxin
DE CRYIA(a)) (Crystalline entomocidal protoxin) (71 kDa crystal protein)
DE (P2 crystal protein) (Mosquito factor).
GN CRY2AA OR CRYIIA(A) OR CRYBI OR CRYII.
OS Bacillus thuringiensis (subsp. kurstaki), and
OS Bacillus thuringiensis (subsp. keryae).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=29339, 33930;
RN (1)
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.kurstaki; STRAIN=HD-1;
RX MEDLINE=89123178; PubMed=2914879;
RA Widner W.R., Whiteley H.R.;
RT "Two highly related insecticidal crystal proteins of Bacillus
RT thuringiensis subsp. kurstaki possess different host range
RT specificities";
RL J. Bacteriol. 171:965-974(1989).
RN (2)
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-26.
RC SPECIES=B.t.kurstaki; STRAIN=HD-263, and HD-1;
RX MEDLINE=88087146; PubMed=3121615;
RA Donovon W.P., Dankosik C.C., Gilbert M.P., Gawron-Burke M.C.,
RA Groet R.G., Carlton B.C.;
RT "Amino acid sequence and entomocidal activity of the P2 crystal
RT protein. An insect toxin from Bacillus thuringiensis var. kurstaki";
RL J. Biol. Chem. 263:561-567(1988).
RN (3)
RP REVISIONS.
RA Donovon W.P., Dankosik C.C., Gilbert M.P., Gawron-Burke M.C.,
RA Groet R.G., Carlton B.C.;
RL J. Biol. Chem. 264:4740-4740(1989).
RN (4)
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.keryae; STRAIN=4A4C / HD-549;
RA Misra H.S., Khairnar N.P., Mathur M., Domellay R.J., Mahajan S.K.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
-1- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
EPITHELIAL CELLS OF BOTH DIPTERAN (ADES AEGYPTI) AND LEPIDOPTERAN
(MANDUCA SEXTA) LARVAE.
CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
SPOROULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
OF THE SPORE COAT.
CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
N-TERMINUS.
CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
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between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its

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CC -----
 DR EMBL; M23723; AAA83516.1; -
 DR EMBL; M31738; AAA22335.1; -
 DR EMBL; AF047038; AAC04867.1; -
 DR PIR; C32053; C32053.
 DR InterPro; IPR005638; endotoxin_C.
 DR InterPro; IPR005639; endotoxin_N.
 DR Pfam; PF03944; endotoxin_C; 1.
 DR Pfam; PF03945; endotoxin_N; 1.
 DR Toxin; Sporulation.
 KW VARIANT 1 MISSING (IN 50% OF THE MOLECULES).
 FT VARIANT 3 N -> S (IN STRAIN 4A4C / HD-549).
 FT VARIANT 409 F -> S (IN STRAIN 4A4C / HD-549).
 FT VARIANT 541 N -> S (IN STRAIN 4A4C / HD-549).
 FT VARIANT 588 S -> P (IN STRAIN 4A4C / HD-549).
 SQ SEQUENCE 633 AA; 70852 MW; 15182F4C78158A4 CRC64;

Query Match 92.0%; Score 3048.5; DB 1; Length 633;
 Best Local Similarity 90.7%; Pred. No. 3.2e-198;
 Matches 574; Conservative 34; Mismatches 24; Indels 1; Gaps 1;

QY 1 MNNVANGRTTICDANNVVAHDPFSEFKSLDTIRKEMEMKRTDHSIYVPIGVTSF 60
 Tb 1 MNNVANGRTTICDANNVVAHDPFSEFKSLDTIRKEMEMKRTDHSIYVPIGVTSF 60
 QY 61 LKKVGSILGKRIILSELMGILIPSSGSTNLMDIIRTEQFLNQRANTDTLARNVALEGI 120
 Db 61 LKKVGSILGKRIILSELMGILIPSSGSTNLMDIIRTEQFLNQRANTDTLARNVALEGI 120
 QY 121 QANIEFNOQVDFNLTQNPVPLSTTSVNTWQQLFRLRPFQVQGYQLLLPFAQA 180
 Db 121 QANIEFNOQVDFNLTQNPVPLSTTSVNTWQQLFRLRPFQVQGYQLLLPFAQA 180
 QY 181 ANMHLSFTRDVYLNADWKGISAATLRTQNLKNTTTEYSANCINTYQTAARGNLRLD 240
 Db 181 ANMHLSFTRDVYLNADWKGISAATLRTQNLKNTTTEYSANCINTYQTAARGNLRLD 240
 QY 241 MLEFRTYMLNVEFYVSLFKYQSLVSSGANLVASGGPQOTOSTSQDMPFLYSLF 300
 Db 241 MLEFRTYMLNVEFYVSLFKYQSLVSSGANLVASGGPQOTOSTSQDMPFLYSLF 300
 QY 301 QVNSVYVNGFSSGARLTQFPNIGLPPTTTTHLLAAVNSGVSQSGDIGAV-ENQNF 359
 Db 301 QVNSVYVNGFSSGARLTQFPNIGLPPTTTTHLLAAVNSGVSQSGDIGAV-ENQNF 359
 QY 360 SCSFPLPPLLPFVRSWLDGSDRGVNTVNMQTSFESTLGLRCGAFTARGNSVYFPD 419
 Db 361 NCSFVLPPLSTPFRVRSWLDGSDRGVNTVNMQTSFESTLGLRCGAFTARGNSVYFPD 420
 QY 420 YFIRNISGVPLVYVNEDELRLPLHYNEINIESPGPGGLRMYVSYNKRNIYVYHN 479
 Db 421 YFIRNISGVPLVYVNEDELRLPLHYNEINIESPGPGGLRMYVSYNKRNIYVYHN 480
 QY 480 GTMIIHAPEDYTGFTISPIHATQVNNQRTFISSEKQNGDSLRFESNTTARYLRNG 539
 Db 481 GTMIIHAPEDYTGFTISPIHATQVNNQRTFISSEKQNGDSLRFESNTTARYLRNG 540
 QY 540 NSVNYLYRVSLSGSTRIRVTINGRYVYTSANNVTNTNDVNNNGARFIDIMNANVASDN 599
 Db 541 NSVNYLYRVSLSGSTRIRVTINGRYVYTSANNVTNTNDVNNNGARFIDIMNANVASDN 600
 QY 600 TAVPLDINVTNPGSTQFELNIMTFYTNLPPIY 632
 Db 601 TAVPLDINVTNPGSTQFELNIMTFYTNLPPIY 633

RESULT 2
 C2AB_BACTK STANDARD; PRT; 633 AA.

AC P21254;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pesticidal crystal protein cry2ab (insecticidal delta-endotoxin
 DE CryIIA(B)) (crystalline entomocidal protoxin) (71 kDa crystal protein).
 GN CRY2AB OR CRYIIA(B) OR CRY2.
 OS Bacillus thuringiensis (subsp. kurstaki).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 NC NCBI_TaxID=29339;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HD-1;
 RX MEDLINE=89123178; PubMed=2914879;
 RA Widner W.R., Whiteley H.R.;
 RT "Two highly related insecticidal crystal proteins of Bacillus
 RT thuringiensis subsp. kurstaki possess different host range
 RT specificities."
 RL J. Bacteriol. 171:965-974 (1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91211618; PubMed=2089222;
 RA Dankocsek C.C., Donovan W.P., Jany C.S.;
 RT "Activation of a cryptic crystal protein gene of Bacillus
 RT thuringiensis subspecies kurstaki by gene fusion and determination of
 RL the crystal protein insecticidal specificity."
 RL Mol. Microbiol. 4:2087-2094 (1990).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BTC002;
 RA Chen Z.Y., Huang D.F.;
 RT "Bacillus thuringiensis Btc002 cry2ab gene."
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 CC - FUNCTION: PROMOTES COLITIDPOSMOTIC LYSIS BY BINDING TO THE MIDGUT
 CC EPITHELIAL CELLS OF LEPIDOPTERAN (MANDUCA SEXTA) LARVAE.
 CC - DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
 CC SPOROGATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
 CC OF THE SPORE COAT.
 CC - MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
 CC N-TERMINUS.
 CC - SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
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QY 1 MNNVANGRTTICDANNVVAHDPFSEFKSLDTIRKEMEMKRTDHSIYVPIGVTSF 60
 Db 1 MNNVANGRTTICDANNVVAHDPFSEFKSLDTIRKEMEMKRTDHSIYVPIGVTSF 60
 QY 61 LKKVGSILGKRIILSELMGILIPSSGSTNLMDIIRTEQFLNQRANTDTLARNVALEGI 120
 Db 61 LKKVGSILGKRIILSELMGILIPSSGSTNLMDIIRTEQFLNQRANTDTLARNVALEGI 120

QY 121 QANREFNOQVDNPLNPTQNPVPLSTSTSVNTMOQLFLNRLPQFRVOGYQLLLPLPFAQA 180
 DB 121 QANVEEFNRQVDNPLNPNRVAVPLSTSTSVNTMOQLFLNRLPQFRVOGYQLLLPLPFAQA 180
 QY 181 ANMHLSFIRDVLANDEMGISAATLTATQNYLKANTYENNYCINTYQAFRGANTRLHD 240
 DB 181 ANMHLSFIRDVLANDEMGISAATLTATQNYLKANTYENNYCINTYQAFRGANTRLHD 240
 QY 241 MLEFRTYFNLNVEEYVSIWLSLFYQSLVSSGANLYASGSGPQOTQSFSTODMPEFLYSLF 300
 DB 241 MLEFRTYFNLNVEEYVSIWLSLFYQSLVSSGANLYASGSGPQOTQSFSTODMPEFLYSLF 300
 QY 301 QVANSNYLVNGFSGARLTOTFPNIGLPGTTTHALLAARNVSGVSGSDI GA VFNQNF 359
 DB 301 QVANSNYLVNGFSGARLTOTFPNIGLPGTTTHALLAARNVSGVSGSDI GASFPNQNF 360
 QY 360 SCSTFLPPLLPFVRWSLDSGDRGVNTVNTMOTESPESTLGLRCGAFARGNSNYPFD 419
 DB 361 NCSTFLPPLLPFVRWSLDSGDRGVNTVNTMOTESPESTLGLRCGAFARGNSNYPFD 420
 QY 420 YFIRNISGVPLVVRNEDLRPLAHNEIRNISPSGTPGGLRAYVSVNRKNNTYAHEN 479
 DB 421 YFIRNISGVPLVVRNEDLRPLAHNEIRNISPSGTPGGLRAYVSVNRKNNTYAHEN 480
 QY 480 GTMTHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQDLSRFGQNTTARTYLRGNG 539
 DB 481 GSWTHLAPDYTGFTISPIHATQVNNQTRTFISEKFGNQDLSRFGQNTTARTYLRGNG 540
 QY 540 NSYNLYLRVSSLGNSITRTVINGRYVTASVNTTNNNDGNGVNDGARFLDIMGVAVASDN 599
 DB 541 NSYNLYLRVSSLGNSITRTVINGRYVTASVNTTNNNDGNGVNDGARFLDIMGVAVASDN 600
 QY 600 TNVPLDINTNTNSGTQFELNIMVFPNLPPIY 632
 DB 601 SDVPLDINTNTNSGTQFELNIMVFPNLPPIY 633

RESULT 3
 ID C2AC BACTU STANDARD; PRT: 633 AA.
 AC 09RMG3;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pesticidal crystal protein cry2ad (insecticidal delta-endotoxin
 DE CryIIA(d)) (Crystalline entomocidal protein) (71 kDa crystal protein).
 GN CRY2AD OR CRYIIA(D) OR CRY2.
 OS Bacillus thuringiensis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_Taxid=1428;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BR30;
 RA Choi S.-K., Shin B.-S., Park S.-H.;
 RT "Nucleotide sequence of a new Bacillus thuringiensis cry2-type gene."
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
 CC EPITHELIAL CELLS OF INSECTS.
 CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
 CC SPOULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
 CC OF THE SPORE COAT.
 CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
 CC N-TERMINUS.
 CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
 CC -----
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DR EMBL: AF200816; AAF05631; -
 DR InterPro: IPR005638; endotoxin_C.
 DR InterPro: IPR005639; endotoxin_N.
 DR Pfam: PF03944; endotoxin_C_1.
 DR Pfam: PF03945; endotoxin_N_1.
 KW Toxin; Sporulation.
 SQ SEQUENCE 633 AA; 70752 MW; 2A582067131B93CB CRC64;

Query Match 88.0%; Score 2916.5; DB 1; Length 633;
 Best Local Similarity 87.2%; Pred. No. 2,56-189;
 Matches 552; Conservative 44; Mismatches 36; Indels 1; Gaps 1;

QY 1 MNNVLANGRITICDANVAVHDPFSEFHKSLDTRKEMEMKRTDHSLYAAYVGVVSF 60
 DB 1 MNSVLNSGRNTICDANVAVHDPFSEFHKSLDTRKEMEMKRTDHSLYAAYVGVVSF 60
 QY 61 LKKYKSLIGKRLISLAKLTIPSGSTNTLMEDILRTEKFLNQKLANDTLRSVNAELTGL 120
 DB 61 LKKYKSLIGKRLISLAKLTIPSGSTNTLMEDILRTEKFLNQKLANDTLRSVNAELTGL 120
 QY 121 QANREFNOQVDNPLNPTQNPVPLSTSTSVNTMOQLFLNRLPQFRVOGYQLLLPLPFAQA 180
 DB 121 QANVEEFNRQVDNPLNPNRVAVPLSTSTSVNTMOQLFLNRLPQFRVOGYQLLLPLPFAQA 180
 QY 181 ANMHLSFIRDVLANDEMGISAATLTATQNYLKANTYENNYCINTYQAFRGANTRLHD 240
 DB 181 ANMHLSFIRDVLANDEMGISAATLTATQNYLKANTYENNYCINTYQAFRGANTRLHD 240
 QY 241 MLEFRTYFNLNVEEYVSIWLSLFYQSLVSSGANLYASGSGPQOTQSFSTODMPEFLYSLF 300
 DB 241 MLEFRTYFNLNVEEYVSIWLSLFYQSLVSSGANLYASGSGPQOTQSFSTODMPEFLYSLF 300
 QY 301 QVANSNYLVNGFSGARLTOTFPNIGLPGTTTHALLAARNVSGVSGSDI GA VFNQNF 359
 DB 301 QVANSNYLVNGFSGARLTOTFPNIGLPGTTTHALLAARNVSGVSGSDI GASFPNQNF 360
 QY 360 SCSTFLPPLLPFVRWSLDSGDRGVNTVNTMOTESPESTLGLRCGAFARGNSNYPFD 419
 DB 361 NCSTFLPPLLPFVRWSLDSGDRGVNTVNTMOTESPESTLGLRCGAFARGNSNYPFD 420
 QY 420 YFIRNISGVPLVVRNEDLRPLAHNEIRNISPSGTPGGLRAYVSVNRKNNTYAHEN 479
 DB 421 YFIRNISGVPLVVRNEDLRPLAHNEIRNISPSGTPGGLRAYVSVNRKNNTYAHEN 480
 QY 480 GTMTHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQDLSRFGQNTTARTYLRGNG 539
 DB 481 GSWTHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQDLSRFGQNTTARTYLRGNG 540
 QY 540 NSYNLYLRVSSLGNSITRTVINGRYVTASVNTTNNNDGNGVNDGARFLDIMGVAVASDN 599
 DB 541 NSYNLYLRVSSLGNSITRTVINGRYVTASVNTTNNNDGNGVNDGARFLDIMGVAVASDN 600
 QY 600 TNVPLDINTNTNSGTQFELNIMVFPNLPPIY 632
 DB 601 SDVPLDINTNTNSGTQFELNIMVFPNLPPIY 633

RESULT 4
 ID C2AC BACTU STANDARD; PRT: 622 AA.
 AC 045743;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pesticidal crystal protein cry2AC (insecticidal delta-endotoxin
 DE CryIIA(c)) (Crystalline entomocidal protein) (70 kDa crystal protein).
 GN CRY2AC OR CRYIIA(C) OR CRYIIC.
 OS Bacillus thuringiensis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_Taxid=1428;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=Shanghai 1 / S-1;
 RX MEDLINE=91340086; PubMed=1651878;
 RA Wu D., Cao X.L., Bai Y.Y., Aronson A.I.;
 RT "Sequence of an operon containing a novel delta-endotoxin gene from
 RT *Bacillus thuringiensis*.";
 RL *Bacillus thuringiensis* Lett. 65:31-36(1991).
 CC -1- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
 CC EPIHELIAL CELLS OF LEPIDOPTERAN LARVAE. HAS LOW ACTIVITY ON
 CC DIPTERAN LARVAE.
 CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
 CC SPOREATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
 CC OF THE SPORE COAT.
 CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
 CC N-TERMINUS.
 CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
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 CC or send an email to license@isb-sib.ch).
 CC EMBL: X57252; CAA00536.1; -
 CC DR PIR: S17402; S17402.
 CC DR InterPro: IPR005638; endotoxin_C.
 CC DR Pfam: PF03944; endotoxin_C_1.
 CC DR Pfam: PF03945; endotoxin_N_1.
 CC KW Toxin; Sporulation; Plasmid.
 CC SEQUENCE 622 AA; 69729 MW; E0B5FAD37B6299 CRC64;
 .SQ
 Query Match 76.8%; Score 2545; DB 1; Length 622;
 Best Local Similarity 78.9%; Pred. No. 2.9e-164;
 Matches 501; Conservative 45; Mismatches 73; Indels 16; Gaps 8;
 QY 1 MANNVANGRTTICDANNVADPFSEHKSIDTRKEWEMKRTDHSIYADIVTYSSE 60
 DB 1 MNNVANGRTTICDANNVADPFSEHKSIDTRKEWEMKRTDHSIYADIVTYSSE 60
 QY 61 LKRVGSLGKRLTSLMGILPSSGNTNMODILSETPOFNSLNDTLAAVNALEGL 120
 DB 61 LKRVGSLGKRLTSLMGILPSSGNTNMODILSETPOFNSLNDTLAAVNALEGL 120
 QY 61 LKRVGSLGKRLTSLMGILPSSGNTNMODILSETPOFNSLNDTLAAVNALEGL 120
 DB 61 LKRVGSLGKRLTSLMGILPSSGNTNMODILSETPOFNSLNDTLAAVNALEGL 120
 QY 121 QANTIRENOQVDNPLNPTQNPVPLSTSVNTMOQLFLNRLPFRVQGIQLLLPLFQA 180
 DB 121 QANVAEFNRQVDNPLNPTQNPVPLSTSVNTMOQLFLNRLPFRVQGIQLLLPLFQA 180
 QY 121 QANVAEFNRQVDNPLNPTQNPVPLSTSVNTMOQLFLNRLPFRVQGIQLLLPLFQA 180
 DB 121 QANVAEFNRQVDNPLNPTQNPVPLSTSVNTMOQLFLNRLPFRVQGIQLLLPLFQA 180
 QY 181 AMNHLSTPRVYLNADENGISAAITRTYQYLNKVTETESVNCINTYQTAFFGLNTRLAD 240
 DB 181 AMNHLSTPRVYLNADENGISAAITRTYQYLNKVTETESVNCINTYQTAFFGLNTRLAD 240
 QY 181 AMNHLSTPRVYLNADENGISAAITRTYQYLNKVTETESVNCINTYQTAFFGLNTRLAD 240
 DB 181 AMNHLSTPRVYLNADENGISAAITRTYQYLNKVTETESVNCINTYQTAFFGLNTRLAD 240
 QY 241 MLEFRTYVFLNVEEYVSWLSLEKYQSLVSSGANLYASGSGPQOTOSTSODMPLYSLE 300
 DB 241 MLEFRTYVFLNVEEYVSWLSLEKYQSLVSSGANLYASGSGPQOTOSTSODMPLYSLE 300
 QY 241 MLEFRTYVFLNVEEYVSWLSLEKYQSLVSSGANLYASGSGPQOTOSTSODMPLYSLE 300
 DB 241 MLEFRTYVFLNVEEYVSWLSLEKYQSLVSSGANLYASGSGPQOTOSTSODMPLYSLE 300
 QY 301 QVNSVYVNGSGARLTQEPNIGLP--GTTTHALLAARVNSGCVSSGSDIG-AVNOQ 357
 DB 301 QVNSVYVNGSGARLTQEPNIGLP--GTTTHALLAARVNSGCVSSGSDIG-AVNOQ 357
 QY 301 QVNSVYVNGSGARLTQEPNIGLP--GTTTHALLAARVNSGCVSSGSDIG-AVNOQ 357
 DB 301 QVNSVYVNGSGARLTQEPNIGLP--GTTTHALLAARVNSGCVSSGSDIG-AVNOQ 357
 QY 358 NFSCTSLPLPLTPPVRSWLDGSGRGVNTVNTWOTSEFSTGLACGAFTRKGSNYF 417
 DB 358 NFSCTSLPLPLTPPVRSWLDGSGRGVNTVNTWOTSEFSTGLACGAFTRKGSNYF 417
 QY 358 NFSCTSLPLPLTPPVRSWLDGSGRGVNTVNTWOTSEFSTGLACGAFTRKGSNYF 417
 DB 358 NFSCTSLPLPLTPPVRSWLDGSGRGVNTVNTWOTSEFSTGLACGAFTRKGSNYF 417
 QY 418 PUYFRINISGVPLVVRNEDLRRPLHYNEIRINISPSGTGGLRKYVNSVNRKNIYVAH 477
 DB 418 PUYFRINISGVPLVVRNEDLRRPLHYNEIRINISPSGTGGLRKYVNSVNRKNIYVAH 477
 QY 418 PUYFRINISGVPLVVRNEDLRRPLHYNEIRINISPSGTGGLRKYVNSVNRKNIYVAH 477
 DB 418 PUYFRINISGVPLVVRNEDLRRPLHYNEIRINISPSGTGGLRKYVNSVNRKNIYVAH 477
 QY 478 ENGTMVHLAPEDYTGFTISHTATOVNQTFTPSKPNQSDSLRPEQONTAAYTARG 537
 DB 478 ENGTMVHLAPEDYTGFTISHTATOVNQTFTPSKPNQSDSLRPEQONTAAYTARG 537
 QY 478 ENGTMVHLAPEDYTGFTISHTATOVNQTFTPSKPNQSDSLRPEQONTAAYTARG 537
 DB 478 ENGTMVHLAPEDYTGFTISHTATOVNQTFTPSKPNQSDSLRPEQONTAAYTARG 537
 QY 469 ENGTMVHLAPEDYTGFTISHTATOVNQTFTPSKPNQSDSLRPEQONTAAYTARG 528
 DB 469 ENGTMVHLAPEDYTGFTISHTATOVNQTFTPSKPNQSDSLRPEQONTAAYTARG 528

QY 538 NGNSYNLYRVSLSAGSTIRTINGRYVTASVNTTNDGVDNGARFLDINMGVVAS 597
 DB 529 NGNSYNLYRVSLSAGSTIRTINGRYVTASVNTTNDGVDNGARFLDINMGVVAS 587
 QY 598 DNTNVPDLIDINTNSGTOPELNMIFPPTLPIY 632
 DB 588 ANTNPVLDIQVTFNGNPOPELNMIFPPTLPIY 622
 RESULT 5
 ID CIBA_PAEPP STANDARD; PRT: 675 AA.
 AC P57091;
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Parasporal crystal protein cry18Aa (Parasporal delta-endotoxin
 DE CryXVIII(a)) (Crystalline parasporal protoxin) (76 kDa crystal
 DE protein).
 GN CRY18A OR CRYXVIII(A). (*Bacillus popilliae*).
 OS *Paenibacillus popilliae* (*Bacillus popilliae*).
 OC Bacteria; Firmicutes; Bacillales; *Paenibacillaceae*; *Paenibacillus*.
 OX NCBI_TaxID=78057;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BP3;
 RA Patel R., Yousten A.A., Rippere K.;
 RT "Detection of two new cry genes in *Paenibacillus popilliae*.";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: BINDS TO THE BRUSH BORDER MEMBRANE VESICLES OF SCAB
 CC LARVAE AND DAMAGES THE GUT WALL SOMEHOW TO ALLOW THE VEGETATIVE
 CC CELLS OF P. POPILLIAE TO ENTER THE HEMOLYMPH (BY SIMILARITY).
 CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
 CC SPOREATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
 CC OF THE SPORE COAT (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
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 CC EMBL: AF169250; AAF69667.1; -
 CC DR InterPro: IPR005638; endotoxin_C.
 CC DR InterPro: IPR005639; endotoxin_N.
 CC DR Pfam: PF03944; endotoxin_C_1.
 CC DR Pfam: PF03945; endotoxin_N_1.
 CC KW Toxin; Sporulation.
 CC FT DOMAIN 101 POLY-LEU.
 CC FT DOMAIN 199 POLY-LEU.
 CC FT DOMAIN 204 POLY-LEU.
 CC SEQUENCE 675 AA; 75848 MW; 823B588B4A81DPS CRC64;
 .SQ
 Query Match 32.8%; Score 1087; DB 1; Length 675;
 Best Local Similarity 38.9%; Pred. No. 7.3e-66;
 Matches 259; Conservative 104; Mismatches 244; Indels 58; Gaps 19;
 QY 2 NNVL--NNGRTTICDANNVADPFSEHKSIDTRKEWEMKRTDHSIYADIVTYSSE 60
 DB 35 NNICSGFMPI---NVRKNP--FRKKTQEFIRREMTMKNSPSLFTAPVIGVATST 88
 QY 61 LKRVGSLGKRLTSLMGILPSSGNTNMODILRETEQFLNORLANTDTLAAVNALEGL 120
 DB 89 LLEMLKKQVQSLLMLMNLPLFNNSTIMEILIRATEQYVQSDLDYTNARVQLEGL 148
 QY 121 QANTIRENOQVDNPLNPTQNPVPLSTSVNTMOQLFLNRLPFRVQGIQLLLPLF 177
 DB 149 KNLRTFNDQIDDF--QNRVEISTPAMIDSINTMOQVFNVLPLFQLSYQQLLLPLF 205
 QY 178 AQAMNHLSTPRVYLNADENGISAAITRTYQYLNKVTETESVNCINTYQTAFFGL-- 234
 DB 178 AQAMNHLSTPRVYLNADENGISAAITRTYQYLNKVTETESVNCINTYQTAFFGL-- 234


```

Db 206 AOGATLHLFIPIIDIIINAGENNIPDAQNTCKRYLKQYVAGYSNALSTYEGAFARARYP 265
Qy 235 NTRLDHMLERTYMLANFEYVSIWLSLFKYOSILVSSGANLYASGSGPOQOTSFSDQMP 294
Db 266 RATLENNLOPKTPTMLANLVLVSIWLSLKKNMLYSTANLXINIGKNKNEBHSISYWP 325
Qy 295 PLYSLQVNSNYLVNGFSGALITOTEPNIGLPGTTTHALLAARVNSGGVSSGDIQAV 354
Db 326 FENSYIQTNSNYLVSGVGIIRWYIANT-FFGGYIOTDMLXNIIISYGVGVNGPKIGVQ 383
Qy 355 FNO-----NFSCSTFLPPLTPFVRSMLDSGDRGVVYVNW 392
Db 384 LSTTELDKQIKQARAMPRTGLDLSFNC-TIANTTPYPAKCPBELSSSTAGTGFI 442
Qy 393 QTESFESTLGLACGAFARAGNS-NYPPDFINISG-VPLVKNEDLRPLHYNINIE 450
Db 443 RSDVPSSEDT-CGAGTGYASAMTSPDYIINISATQVDGINIDI-TPLCFGEDEAIT 500
Qy 451 SPSCGTGGLRAYVSVNHRKNIIYVAHENGTMHILAPEDYGTISPIHATQVANNQRTF 510
Db 501 STHGIV-----NKVIAYVRKANLAGINONGTMHQAIPDGTFTVPLHLASFTHBEAH 555
Qy 511 ISEKFGNODSLREFQSTTKARTLTNGNS-YNLYERVS-IGNSTIRVITNGRYTAS 568
Db 556 IQENYVGSQDSRLTGPTTALTYMLSGDRRTTYKLVLKVGIVTRITAKVGNISIGY-LE 614
Qy 569 NVATTTNDGVNDGARFLDINNGVNASD-NTNVPDINVTNFGSOTPELMNIMPFTN 627
Db 615 YINTVNNQGITDNSKQPEPERPITIDACTIVLEFASIN-----FDLMNLIPIFY 670
Qy 628 LPPIY 632
Db 671 DTPY 675

RESULT 6
CICA_PABPP STANDARD; PRT; 706 AA.
AC 043558;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Parasporal crystal protein cry18aA (Parasporal delta-endotoxin
DE Cryxviii(a)) (Crystalline parasporal protoxin) (79 kDa crystal
DE protein).
GN CRY18AA OR CRYXVIII(A) OR CRYBP1.
OS Paenibacillus popilliae (Bacillus popilliae).
OC Bacteria; Firmicutes; Bacillales; Paenibacillaceae; Paenibacillus.
OX NCBI_TaxID=78057;
RN (1)
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=H1 / subsp. melolonthae;
RX MEDLINE=97352693; PubMed=9209052;
RA Zhang J., Hodgman T.C., Krieger L., Schaefer W., Schaefer H.U.,
RA "Cloning and analysis of the first cry gene from Bacillus popilliae.";
RT J. Bacteriol. 179:4336-4341 (1997).
RL -1- FUNCTION: BINDS TO THE BRUSH BORDER MEMBRANE VESICLES OF SCARAB
RL LARVAE AND DAMAGES THE GUT WALL SOMEHOW TO ALLOW THE VEGETATIVE
RL CELLS OF P. POPILLIAE TO ENTER THE HEMOLYMPH. ACTIVE ON
RL M. MELOLONTA.
CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
CC SPORELIATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
CC OF THE SPORE COAT (BY SIMILIARITY).
CC -1- SIMILIARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
CC -----
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DR EMBL: X99049; CAA67506.1; -.
DR InterPro: IPR001178; Endotoxin.
DR InterPro: IPR005638; endotoxin_C.
DR InterPro: IPR005639; endotoxin_N.
DR Pfam: PF00555; endotoxin_1.
DR Pfam: PF03944; endotoxin_C; 1.
DR Pfam: PF03945; endotoxin_N; 1.
DR Toxin; Sporulation.
KW CONFLICT 670 670 T -> F (IN REF. 1; AA SEQUENCE).
SQ SEQUENCE 706 AA; 79034 MW; 9172B949BE499CID CRC64;

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Query Match 32.6%; Score 1080; DB 1; Length 706;
Best local similarity 38.4%; Pred. No. 2,36-65;
Matches 264; Conservative 96; Mismatches 233; Indels 94; Gaps 21;

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Qy 2 NNVLAN-----GRITTCDA-----YNAVADPFSPFHKSLDTRKEMWEMKRTD 45
Db 58 NNDNNNDATCELDGPIPIIDNNTICSTDEPTPIVWVRTP--FKKSTQELIREWTEWKENS 115
Qy 46 HSLYVAPIVGVSSFLKXKYSGLIKRTLSLWGLIFSGSTNLMQDILARETQPLANQL 105
Db 116 PSLFTPALVGVVSEFLQSLKQATSFLLKTLTDLPNNSSLTMEILRATQVQDEL 175
Qy 106 NTDTLARYNAELLEGQANIREFNQVDNFINPTONVPLSITSSVNTWQQLFLARLPQR 165
Db 176 DDTANRVSEQLVGLKXNLTTFNDQVEDPQNVGSIPLAIIIDSINTMQQLFVNRLLPQR 235
Qy 166 VCGYQLLLPLFAQANMLHSTRVUNLNDENGISAATLRTQYKLTNTTYSNYCIN 225
Db 236 VSGYQVLLPLFAQATLHFLTRDVIIINDENITFAQLNTYTFEKEVIAEYSVYALS 295
Qy 226 TYQTAFRGLNTR-----LHDMLEERTYMLANFEYVSIWLSLFKYOSILVSSGANLYASG 279
Db 296 TYDDGR---TRFYPRNTLEDMLQKTFMTLNLALDVISIWLKXVNLVYSTANLYNIG 352
Qy 280 SSGQQTOSFTSQDMPFLYGLFQVNSNYLVNGFSGALITOTEPNIGG-----LPGTTTH 333
Db 353 DNKNVGAIPISYGPFPNSYIQTKSNVYLVSGVIGARFYTIVIGRYLHDDKNIIT- 411
Qy 334 ALLAARVNSGVSDDIGAVN-----QNFSCSTFLP-DLTP 371
Db 412 -----YVGGTQGPNTIGVQSTTELDLKKQOATRDLVDPFPIANOMLPNRTNP 463
Qy 372 -FVRSMLDSG-SDRGVNTVNTWQTESFESTGL-RCGAFTRAGNSVPPDYIRNISGV 428
Db 464 FYATSLVESRYSSIGLKKDVFSK--DSTGLGNPGAMTS-----YDYVITNISAT 515
Qy 429 PLVVENEDLRPLHYNIEINIESPSGTGGLRAYVSVNHRKNIIYVAHENGTMHILAP 488
Db 516 VOINGENTDTPLYPKENRPITSTGV-----NKVIAYVRKANLAGINONGTMHQAIP 570
Qy 489 DYTGTISLPIHAYVANNQRTFISKKGNOGSLRPEQNTARTYLRGNG-NSYULYR 547
Db 571 DGTGTVSELPBSA--NTTSTIKENTGNSGSLH--KQGYLHMLSGNGQRYLVLR 627
Qy 548 VSSLGNSITRTVINGRYVTSVNTTNDGVNDGARFLDINNG--VVASDNTVPLD 605
Db 628 LSGAAN---QIKLQSTPITSIVAFDSTINNEGITDNSKQPEPSTFVIAPEQ-----E 679
Qy 606 INVTNFGSOTPELMNIMPFTNLPPIY 632
Db 680 ILYFEGVGLDMLNLIPLADDTPLY 706

RESULT 7
CICA_PABPP STANDARD; PRT; 695 AA.
AC P57092;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Parasporal crystal protein cry18aA (Parasporal delta-endotoxin
DE Cryxviii(a)) (Crystalline parasporal protoxin) (78 kDa crystal

```

DE protein.
 GN CRY18CA OR CRYXIIIC(A).
 OS Paenibacillus popilliae (Bacillus popilliae).
 OC Bacteria; Firmicutes; Bacillales; Paenibacillaceae; Paenibacillus.
 OX NCBI_TaxID=78057;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 14706;
 RA Patel R., Yousten A.A., Rippere K.;
 RT "Detection of two new cry genes in Paenibacillus popilliae."
 RU Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: BINDS TO THE BRUSH BORDER MEMBRANE VESICLES OF SCARAB
 CC LARVAE AND DAMAGES THE GUT WALL SOMEHOW TO ALLOW THE VEGETATIVE
 CC CELLS OF P. POPILLIAE TO ENTER THE HEMOLYMPH (BY SIMILARITY).
 CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
 CC SPOULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
 CC OF THE SPORE COAT (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
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 CC -----
 CC EMBL, AF169251; AAR89668.1; -
 DR InterPro; IPR005638; endotoxin_C.
 DR InterPro; IPR005639; endotoxin_N.
 DR Pfam; PF03944; endotoxin_C_1.
 DR Pfam; PF03945; endotoxin_N_1.
 KW Toxin; Sporulation.
 SQ SEQUENCE 695 AA; 78259 MW; 406AC9154D75E070 CRC64;
 Query Match 32.4%; Score 1073.5; DB 1; Length 695;
 Best Local Similarity 37.6%; Pred. No. 6.2e-65;
 Matches 256; Conservative 115; Mismatches 241; Indels 69; Gaps 18;
 2 NNV-----LNNGRITTCIDAY-----NVVADPFSEHKSDITRKEMWKRTDHS 47
 34 NNVNNGDLVNLGLPIDNNFGSNGFIPRVNTRKDP--PRKKTQEFIRFEMTEWKEKAS 91
 48 LVVAPIGVTSSELLKKGSLGKRIISELMGIFPSGSTNMODIIRTEQPLNORLT 107
 92 LFTAPIGVITSTLEALKKLVAGKVLMSLTNLPFNSTIMEIIRATEOYIPEQDLT 151
 108 DTLARVNALEGLQANIRENQOVNPLNPTONPVLSTTSVNTMOQLFLNLPQFRVQ 167
 152 VTMNVRVSELEGLKNDLRTFNQIDDFLQNRVGISPLAIIIDISNTMOQLFVNRLPQFVS 211
 168 GVOULLLPLPAQANMHLSPIDVYLNADENGLSATLTATYONVLYKQYTEVSNVCINTY 227
 212 DDQVLLPLPFAQVATLHLTFVDDIITNADENIPERQNLTVYKRYKQYVAQSNVNLSTY 271
 228 QTAFRG-----LNTRLHMLEFTYVFLNVEEYVSIWLPKYQSILVSSGANLYVSSGSPQ 283
 272 EEARFARFYPENT-VERMLEFTFMTLVNLDIVSMSSLKLYNLVSTANLYGDNKV 330
 284 QROSTFSDMPFLYSLFQVNSNYVLNNGSARLQTFEPV-----IGG 325
 331 NGEYSISYMPFENTYIYQKSNYVLVSGVSGVAMSWSTNPPFGEYIQDHLNNTASYSIG 390
 326 LFG-----TTTHALLAARVNSGVSAGDIGNVQNSGSTEPLLPFVRSWL 377
 391 VNGPQIGQALSTTELQVQQ-----ARAADI PVDFTQIPINCTLRNLEVPYATRF 443
 378 DSGSRGAVNTVTWQTESFESEGLRCGAF-ARGNSVPEPDYVNTINISG-VELAVNRE 435
 444 NELTSLGTAGVGGFVRSDFISNDV-CGLGNTNSSGQTFPDYVNTINISATYQVAGVNT 502
 436 DLRRPLAHNEIRNIESPSGTGGRLAVVNSVHNKNNIYAVHEN--GTMTHLAPEDYTG 493

DB 503 DI-SPLFGENRAITSTNGV-----NKVIAIYNKTN-YDFTNIRGTIVHEAFDSTG 555
 QY 494 TISPIHATQVNNQRTFISEKQNGSDSLRPEOSNTARVTL-RGNGSNVYLVRVSSIG 552
 DB 556 TISPELHDTVNIINSYLYIQANTYNNQSDSLR-IRNAIKRSLAARSIVYLVLRVSGTA 614
 QY 553 NSTIRVTINGRVYASNVNTTNDGVNDNGARPLDINMGVNVASDNTNVPDLINT-EN 611
 DB 615 SSIYAIEYVPGASANOINTGNEGVNIDNDSKFDLIFPTFVSVGTARELQVSGAT 674
 QY 612 SGQFELANIMVFNPLPPIY 632
 DB 675 TSPEDIMIIILIPINDVPLX 695
 RESULT 8
 CBA_BACCT STANDARD; PRT; 643 AA.
 ID CBA_BACCT
 AC P21256;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pepticidal crystal protein cryIIAa (insecticidal delta-endotoxin
 DE cryIIAa(a)) (crystalline entomocidal protoxin) (72 kDa crystal protein).
 GN CRYIIA OR CRYXIIA(A) OR CRYIIV OR CRYD.
 OS Bacillus thuringiensis (subsp. israelensis).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1430;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89008093; PubMed=2902069;
 RA Donovan W.P., Dankocsik C.C., Gilbert M.P.;
 RT "Molecular characterization of a gene encoding a 72-kilodalton
 RT mosquito-toxic crystal protein from Bacillus thuringiensis subsp.
 RT israelensis";
 RT J. Bacteriol. 170:4732-4738(1988).
 CC -1- FUNCTION: PROMOTES COLITODSMOTIC LYSIS BY BINDING TO THE MIDGUT
 CC EPITHELIAL CELLS OF MOSQUITOS.
 CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
 CC SPOULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
 CC OF THE SPORE COAT.
 CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
 CC N-TERMINUS.
 CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL, M31737; AAA2352.1; -
 DR PIR; A43647; A43647.
 DR InterPro; IPR005639; endotoxin_N.
 DR Pfam; PF03945; endotoxin_N_1.
 KW Toxin; Sporulation.
 SQ SEQUENCE 643 AA; 72348 MW; 64CA35495409B74E CRC64;
 Query Match 10.2%; Score 336.5; DB 1; Length 643;
 Best Local Similarity 23.1%; Pred. No. 2.9e-15;
 Matches 167; Conservative 98; Mismatches 257; Indels 201; Gaps 34;
 27 EHKSLDTRKEMWKRTDHSLY-----VAP--IVGVSSFLKKGSLIGRIILSE 76
 DB 2 EDSISDLTSLIV-----NETDFPLNNTTEPTIAPLIVAVIAQYATLAIQKAAKAASF 57
 QY 77 LMGILFSSGNTLMODIIRTEQFLNQRANTDTLARVNALEGLQANIRENQOVNPLN- 135
 DB 58 VLSLIFPGSGAPATMKATVETETLIQKLSQDRVNIINAAYRG-----ILEVSDVFDVYIK 113
 QY 136 NPTONPVLPLSTSSVNTMOQLFN-----RLPQFRVQGYQLLLPLFAQANMHLSTFI 188

DB 114 QGPTPA-----TAKGYFNLGALITGRLPQFVQTECVSIALFTQWCTLHTLL 164
 QY 189 RDVVLNADWDGISAATRTYQNYLKYTTEYVNCINTYQTA-RLGNTLRLHMLDEPRY 247
 DB 165 KDGLAGSAMGFTQADVDSFKLPNOKYLDYTHLMEMYTEERGRCKSLKDLGTLTRM 224
 QY 248 MFLNFEVYSIWSLFKQSLVSSGANLYASGSGPOQTGFTSQDMPFLYSLFQVNSN-- 305
 DB 225 CNLYVFPFAEAMSLMRFBGKLOSLSL-----MDVGVGSIPIVANNEM 267
 QY 306 ----YVNGSGARLTQTFPNIGLPGTTTHALLARVYNSG-----GVSSGDIAVY 355
 DB 268 GGLVYKLMGVEVNGRLTVKENY-----SFTMEPADIPARENIRGVHPIYDSSGLTWIG 323
 QY 356 N---QNFSGSTFLPLILTPVRSWLDSDGKGVNYTYNQ----- 393
 DB 324 NGRTNNENFAD-----NNGNEIMEVRTQTFQNNENPIAPRDIINQTLTA 369
 QY 394 -----TESFESTL---GLRGAFTARGN-----SNY--PDDYFTINI 425
 DB 370 PADADLFFKNADINVKFTQWFOSTLYGNMILGQTVLSRGTLIPRYLAVDGYTRAI 429
 QY 426 SGVPLVYR---NEDLRRLPHNRIKNSPSG-----TPGGLRNVVSVHKNKNTYA 475
 DB 430 SACEKGVSLAYHDL-TTLTYNRI-EYDSPTTENIIVGAPADMTQDF-----YSKKS--- 479
 QY 476 VHENGTMHLAPEDYGTFTISPIHATOVNQTFTISEKQNGD-SLRPFSQ--WTTR 532
 DB 480 -----HYLSEFNDSYVIALQFAVSD--RSFLDPDQATGDSIKFARTFISNEAK 529
 QY 533 YTLRNGNSYMLYRVSLSGNTIRPTNGVYTAASVNTTNNNGVNDGAPFLDING 592
 DB 530 YSIRLN-TGFMTATRYKI---IRVRPYTL--PACIRVQNSGNN---PMLGSFTA 578
 QY 593 NV-----VASDNTVPLDINV-TPNSGTFEIMNIMEV-----PTNL 628
 DB 579 NNPMPVDFVTDAFTFNDLGITTSSTNALFSSISDSINGSEWYLSQFLVKESAFRTQI 638
 QY 629 PPI 631
 DB 639 NPL 641

RESULT 9
 C1A_BACTK STANDARD; PRT: 719 AA.
 AC Q45752; P71092; Q45750; Q45751; Q45756;
 AC 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pepticidal crystal protein cryIIa (insecticidal delta-endotoxin
 DE cryII(a)) (Crystalline entomocidal protoxin) (81 kDa crystal protein).
 GN CRYIIA (A) OR CRYV OR CRYVI OR CGCGYV.
 OS Bacillus thuringiensis (subsp. kurstaki).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 NX NCBI_TaxID=29339;
 RX STRAIN=DSIR732;
 RC STRAIN=DSIR732; PubMed=8517758;
 RA Gleave A.P., Williams R., Hedges R.J.;
 RT "Screening by polymerase chain reaction of Bacillus thuringiensis
 RT serotypes for the presence of cryV-like insecticidal protein genes and
 RT characterization of a cryV gene cloned from B. thuringiensis subsp.
 RT kurstaki".
 RL Appl. Environ. Microbiol. 59:1683-1687 (1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CHCC4835;
 RX MEDLINE=92269582; PubMed=1588820;
 RA Taylor R., Tippet J., Gibb G., Pells S., Pike D., Jordan L., Ely S.;
 RT "Identification and characterization of a novel Bacillus thuringiensis

RT delta-endotoxin entomocidal to coleopteran and lepidopteran larvae.",
 RL Mol. Microbiol. 6:1211-1217 (1992).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HD-1;
 RX MEDLINE=95314293; PubMed=7793960;
 RA Shin B.-S., Park S.-H., Choi S.-K., Koo B.-T., Lee S.-T., Kim J.-I.;
 RT "Distribution of cryV-type insecticidal protein genes in Bacillus
 RT thuringiensis and cloning of cryV-type genes from Bacillus
 RT thuringiensis subsp. kurstaki and Bacillus thuringiensis subsp.
 RT entomocidis".
 RL Appl. Environ. Microbiol. 61:2402-2407 (1995).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AB88;
 RX MEDLINE=96178985; PubMed=8606196;
 RA Koeltzcha K., Warren G.W., Mullins M., Mullins A.D., Palekar N.V.,
 RA Craig J.A., Koziel M.G., Estruch J.J.;
 RT "Cloning of a cryV-type insecticidal protein gene from Bacillus
 RT thuringiensis: the cryV-encoded protein is expressed early in
 RT stationary phase".
 RL J. Bacteriol. 178:2141-2144 (1996).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=61;
 RA Selvapandian A., Bhattacharya R.K.;
 RT "Isolation, cloning and expression of cryV gene".
 RL Submitted (Oct-1996) to the EMBL/GenBank/DBD databases.
 CC -1- FUNCTION: PROMOTES COLONIZATION OF THE MIDGUT
 CC EPITHELIAL CELLS OF CERTAIN COLEOPTERAN AND LEPIDOPTERAN SPECIES.
 CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
 CC SPOULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
 CC OF THE SPORE COAT.
 CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
 CC N-TERMINUS.
 CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
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CC EMBL M98544; AAA22354.1;
 CC EMBL X62821; CAA4633.1;
 CC EMBL I36338; AAC3699.1;
 CC EMBL I49391; AAB00958.1;
 CC EMBL Y08920; CAA70124.1;
 CC PIR I39815; I39815.
 CC PIR S25383; S25383.
 CC HSP: P02965; ICY.
 CC InterPro: IPR001178; Endotoxin.
 CC InterPro: IPR005638; endotoxin_C.
 CC InterPro: IPR005639; endotoxin_N.
 CC Pfam: PF00555; endotoxin_1.
 CC Pfam: PF03944; endotoxin_C_1.
 CC Pfam: PF03945; endotoxin_N_1.
 CC Toxin; Sporulation.
 FT VARIANT 159 233 K -> R (IN STRAIN 61).
 FT VARIANT 233 233 D -> Y (IN STRAIN CHCC4835 AND HD-1).
 FT VARIANT 443 443 A -> V (IN STRAIN AB88).
 FT VARIANT 711 712 KQ -> NE (IN STRAIN HD-1 AND 61).
 SQ SEQUENCE 719 AA; 81216 MW; 3627E5A6C25DAF5 CRC64;

Query Match 9.9%; Score 327.5; DB 1; Length 719;
 Best Local Similarity 22.8%; Pred. No. 1.4e-14;
 Matches 162; Conservative 103; Mismatches 271; Indels 173; Gaps 32;
 21 HDSPSEHK-----SDTTRKWK-MEKRTYD-----SLY-VAP----- 52

Db 9 H0SESSNAKYDKISTDLSKNETDI ELQINHEDCIKRSEYENVEPVSASTIQTGICIG 68
 QY 53 -YGVTSFLLKRVYSLIGKRLISELMGLIFPSGSTNLMODILRETEQFLNORLNTDTLA 111
 Db 69 KIIGTIGVPAQVASTV-SFLLGELM-----FKGK-NOMELFMEHEEELINOKISTAYR 122
 QY 112 RVNAHEGLQANIREFNOQVDFNLTQNPVPLST--SVYTMQQLFELNLPORVQGYO 170
 Db 123 KALTDKLGDAVLAVYHDSLESVGNRRNTKASVWSQYITALELMEFVOKLPSRVSGBE 182
 QY 171 LLLPLFPAOANMHLSPFRDVLNADENGISATLRTYONLKNYTESNYCINTYQTA 230
 Db 183 VPLLPFYAQAANLHLLLRDASIFGKEMGLSSSEISTFYRQVERAGSDHCVMYSTIS 242
 QY 231 FRGL-NTRLHDL-----EFRTYMLNFEYVSWLSLFFKQSLVSSGANL-----YASGSGP 282
 Db 243 LNNRGTAESWVRYNQFRDMLTMDLVALPSPSYDTQMPYIKTNAOLTEVYTDALGT 302
 QY 283 QQTQ-SPTSQDM-----PFL-----YSLFQVNSN-YVLNGFSG 313
 Db 303 VHPSPSTSTWYNNNAPSFSALFAAVRNPHLLPFLQVYITSLSRMSNTQYNNMVG 362
 QY 314 ARLTQTFPNIIGLPETTTTHALLAARVNSGVSSGDIQAVNQNFCSTFLPPLTPPV 373
 Db 363 HRL--NFRIGGLTINTST-----QSTNTSINVTLPFT 394
 QY 374 RSWLDGSGDRGVNTVT-----NMQ--TESFESTGLRGCAFTARGNSNTPD 419
 Db 395 SRDVFRTESLAGLNLFLQPVNGVPRVDFMFWVHPPIAS-----DMFYYPG 441
 QY 420 YFRTNLSGVLAVYRNEDLRPLHYNELRNIESPGTGGALAVYVWVHRKNKIYA-VHE 478
 Db 442 Y-----AGISTQLODSENELEPPEATGQPNYESHRLSHIG--LISASHVKAALYSWTHR 494
 QY 479 NGTMHLAPEDYTGFTTSPHATOV-----NNQRTTISKEGK--NOGSLAFESQNTA 531
 Db 495 SA-----DRTN-TIEPNSITQIPVKAFLNLSGGAAVRGPGFTGGDLR--RTNNGT 543
 QY 532 RYTLRGNGN-----SNLYLRVSSLNGSTRITARYTASNNVTNTTNDVNDNGARF 566
 Db 544 FGDIRVNINPPFAQRYRIRIXASTDLOPHNSINGKAINOGNSATNMR-----GED 596
 QY 587 LDINMGAVVASDNTNVPDINT-----FNSGTQFLMAMVPLNL 628
 Db 597 LDYKTFRTVGTTPPSFILDVOSTFTIGAMNFSNGEYVIDRIEFPVEV 645

RESULT 10
 CLBD_BACT2
 ID CLBD_BACT2 STANDARD; PRT; 1231 AA.
 AC Q9ZAS5;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Peptidicidal crystal protein cryIbd (insecticidal delta-endotoxin
 DE CRYIb(d) (CryIb(d) toxin) (140 kDa crystal protein).
 GN CRYIb OR CRYIb(d) OR CRYIb OR CRYIb.
 OS Bacillus thuringiensis (subsp. wuhanensis).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=52024;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HD-525;
 RX MEDLINE=20153386; PubMed=10688690;
 RA Kuo W.-S., Lin J.-H., Tzeng C.-C., Kao S.-S., Chak K.-F.;
 RT "Cloning of two new cry genes from Bacillus thuringiensis subsp.
 RL wuhanensis strain"; 40:227-232(2000).
 CC CURR. Microbiol. 40:227-232(2000).
 CC FUNCTION: PROMOTES COLLOIDOTIC LYSIS BY BINDING TO THE MIDGUT
 CC EPITHELIAL CELLS OF LEPIDOPTERAN LARVAE. TOXIC TO PLOTELLA
 CC XYLOSTELLA.
 CC -!- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
 CC SPOULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART

CC OR THE SPORE COAT.
 CC -!- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
 CC N-TERMINUS.
 CC -!- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
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 CC
 CC DR EMBL; U70726; AAD10292.1; -
 CC DR HSSP; P02965; ICY.
 CC DR InterPro; IPR001178; Endotoxin.
 CC DR InterPro; IPR005638; endotoxin_C.
 CC DR InterPro; IPR005639; endotoxin_N.
 CC DR Pfam; PF00555; endotoxin_1.
 CC DR Pfam; PF03944; endotoxin_C_1.
 CC DR Pfam; PF03945; endotoxin_N_1.
 CC DR Toxin; Sporulation.
 CC KW
 CC SQ SEQUENCE 1231 AA; 139654 MW; 129A0371CDDEE52 CRC64;
 Query Match 9.9%; Score 327.5; DB 1; Length 1231;
 Best local similarity 23.3%; Pred. No. 2,9e-14;
 Matches 155; Conservative 101; Mismatches 249; Indels 161; Gaps 29;
 QY 52 PIVGVTSFLLKRVYSLIGKRLISELMGLIFPSGSTNLMODILRETEQFLNORLNTDTLA 111
 Db 73 PFAGQIASRFSYFLV-----ELW--RDPELELHEVQLRQVYNTNTN 118
 QY 112 RVNAHEGLQANIREFNOQVDFNLTQNPVPLSTISVYTMQQL-FLNLPORVQGYO 170
 Db 119 TALARLEIGRGVWSYQALLETMLNDRDARSIIILERYVALLEIDITTAIPFLIRNNE 178
 QY 171 LLLPLFPAOANMHLSPFRDVLNADENGISATLRTYONLKNYTESNYCINTYQTA 230
 Db 179 VPLMVTQAANLHLLLRDASIFGSEWGNASDVNOYQEOGIRTEIYSNHCWYNTNG 238
 QY 231 FRGL-NTRLHDL-----EFRTYMLNFEYVSWLSLFFKQSLVSSGANL-----YASGSGP 282
 Db 239 LNNRGTAESWVRYNQFRDMLTMDLVALPSPSYDTYINTSAQLTREIYTPPIGR 298
 QY 283 QQTQ-SPTSQDM-----PFL-----YSLFQVNSN-YVLNGFSG 313
 Db 299 TNAPSGFASITWENNAPSFALEAATFRPHLLDPEQULIYSASSMSSTQHMVYWG 358
 QY 314 ARLTQTFPNIIGLPETTTTHALLAARVNSGVSSGDIQAVNQNFCSTFLPPLTPPV 373
 Db 359 HRL--NFRIGGLTINTST-----QSTNTSINVTLPFT 394
 QY 374 RSWLDGSGDRGVNTVT-----NMQ--TESFESTGLRGCAFTARGNSNTPD 419
 Db 392 SRDVFRTESLAGLNLFLQPVNGVPRVDFMFWVHPPIAS-----DMFYYPG 441
 QY 420 YFRTNLSGVLAVYRNEDLRPLHYNELRNIESPGTGGALAVYVWVHRKNKIYA-VHE 478
 Db 442 Y-----AGISTQLODSENELEPPEATGQPNYESHRLSHIG--LISASHVKAALYSWTHR 494
 QY 479 NGTMHLAPEDYTGFTTSPHATOV-----NNQRTTISKEGK--NOGSLAFESQNTA 531
 Db 495 SA-----DRTN-TIEPNSITQIPVKAFLNLSGGAAVRGPGFTGGDLR--RTNNGT 543
 QY 532 RYTLRGNGN-----SNLYLRVSSLNGSTRITARYTASNNVTNTTNDVNDNGARF 566
 Db 544 FGDIRVNINPPFAQRYRIRIXASTDLOPHNSINGKAINOGNSATNMR-----GED 596
 QY 587 LDINMGAVVASDNTNVPDINT-----FNSGTQFLMAMVPLNL 628
 Db 597 LDYKTFRTVGTTPPSFILDVOSTFTIGAMNFSNGEYVIDRIEFPVEV 645

```

243 LUNRI.BGTNAESWVRN--OEPBMTI.MT DI IAI EPEYDPMVDT DTCOI ENNNNNNNNN 000

```

DR EMBL; U07642; AAA82114.1; -
DR PIR; I40590; I40590.

GN CRYICA OR CRYIC(V).
 OR Bacillus thuringiensis (subsp. colworthi)).
 CC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1442;
 RN RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RX STRAIN=BT026184;
 RX MEDLINE=66141404; PubMed=8572715;
 RA Lambert B., Byssse L., Dacoc C., Jansens S., Pien S., Saey B.,
 RA Seutin J., Van Audenmove K., Van Rie J., Van Vliet A., Piferen M.,
 RA "A Bacillus thuringiensis insecticidal crystal protein with a high
 RT activity against members of the family Noctuidae."
 RL Appl. Environ. Microbiol. 62:80-86(1996).
 CC -1- FUNCTION: PROMOTES COLICIDOSPOTIC LYSIS BY BINDING TO THE MIDGUT
 CC EPITHELIAL CELLS OF LEPIDOPTERA LARVAE. HAS A FAIRLY BROAD
 CC SPECTRUM OF ACTIVITY AGAINST MEMBERS OF THE FAMILIES PYRALIDAE,
 CC PLUTELLIDAE, SPHINGIDAE, AND NOCTUIDAE. IT IS THE FIRST
 CC INSECTICIDAL CRYSTAL PROTEIN WITH ACTIVITY AGAINST CUTWORMS. NO
 CC ACTIVITY IS OBSERVED AGAINST SOME BEETLES, SUCH AS COLORADO POTATO
 CC BEETLE.
 CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
 CC SPOULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART OF
 CC THE SPORE COAT.
 CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE N-
 CC TERMINUS.
 CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
 CC -----
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 CC or send an email to license@1sb-sb.ch).
 CC
 CC EMEDL: Z37527; CAAB5764.1; -.
 CC PIR: A59350; S49247.
 DR HSSP: P07130; IDLC.
 DR InterPro: IPR001178; Endotoxin.
 DR InterPro: IPR005638; endotoxin_C.
 DR InterPro: IPR005639; endotoxin_N.
 DR pfam: PF00555; endotoxin; 1.
 DR pfam: PF03944; endotoxin_C; 1.
 DR pfam: PF03945; endotoxin_N; 1.
 DR toxin; Sporulation.
 KW toxin; Sporulation.
 SQ SEQUENCE 1157 Aa; 129775 MW; C364391EF7PDFB8A CR664.

Query Match 9.3%; Score 307; DB 1; Length 1157;
 Best Local Similarity 23.4%; Pred. No. 6,4e-13;
 Matches 163; Conservative 87; Mismatches 215; Indels 232; Gaps 34

QY 52 PIVGVTSGLLAKKVGSLIGRIISLWCLFPSSGSNTIMODILREPOFLRNLTDTLA 111
 DB 87 PFSQIVSYR-----QPLINTLM-----PNDRIATENAFMGQBELVNOIREFARN 133
 QY 112 RVNNELEGIANIREFNOQVDFL--NPQNPVLSTSSVTNMQQ-FLARLPQRYQ 167
 DB 134 QALARIQAGDSFNVYORSIQMLNDARDNTN--LSVVRQPTALDLFVNAIPLEFVN 190
 QY 166 GYQILLLEPAQANMHLSTIRVYLVNDEWGISATLETTRYQNLKAYTTEYSNCTNY 227
 DB 191 GQGVPLLSVYAAQVNLHLIKRKSIFEGMGQPTQGEISITYYDQDELTAKTNYCETWY 250
 QY 228 QTA---FRGIANT---RIHDMLEFRTYFLNVEBYVSIWSLPTKQSLIYSSGAMNYASGS 260
 DB 251 NTGDLRIKRGNTSEWLRH--QFRENTIIVLDVV--ALFPTYDV-----RLYPTGS 298
 QY 281 GPOQNGS-FRS-----QMW-----PLY-----S 298
 DB 299 NFQILTRVYTDIPVNPANVGLCRKMGNTYNTFSELMNAFIRPHLPRLNSLTISNN 358
 QY 359 LFQVNSNYVLNFGSARLTQTFNIGLPG-----TTTHALLAARNVYGGVSGDGLG 352

Db 359 REPVSNNF-MDYSGHTLRSLYNDASVQEDSYGLITTTTRATINPGVGTNRIBESTAVDF 417
 QY 353 -----AVFNONFSCSTFLPLLPPLTPFVSMDSGD---RGVNVN---TMMQTESSESTLG 402
 Db 418 RSALIGIYGVN-----RASFPVGGIPLNITTSBPANGCRULYTHNDELPEDEST-- 465
 QY 403 LRCAAFARAKNSNYPEDY-----FINNISGVLV---RNEDIRRLPHNIEIRNIESPS 453
 Db 466 ---GSSTHRLSHVTFEFSFQTAQASINAGSVPTVWTRRDVLNITIPNRITQLP--- 519
 QY 454 GTPGGLRAYVSVHNRKNNIYAIVHNGTMTLHAPEDYGTFTSPHATQVNNQGTTFISE 513
 Db 520 -----LVKA-----SAPVSGITVLAKP---GFI----- 539
 QY 514 KFGNQGSLAFEGSNTTARTYLRKNGNS-----YNIYLRVSSLGNTSTIRVTIN---GRV 564
 Db 540 ---GGGILRRRTNNGTFG--TLRTVNSPLTQOYLRVRFASSTNFSIIVLGGVSIQDV 593
 QY 565 YTAGSNV-----TTT-----NNDGVNDNGARPLD--- 588
 Db 594 RLGGSTNRGQELTFESFTFRFTTGGPFNPFTFQAGELITVNAEGVSGEGYIYDRIE 653
 QY 589 ---INMGNVASD-----NTNVPLDINVT 609
 Db 654 IVPVNPAREAEDELAKKAVASLFTETRDGLQVNV 690
 RESULT 14
 ID C7AB BACUA STANDARD; PRT; 1138 AA.
 AC 045707:
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pesticidal crystal protein cry7Ab (insecticidal delta-endotoxin
 DE CryVIIA(b)) (Crystalline entomocidal protoxin) (130 kDa crystal
 DE protein).
 GN CRY7AB OR CRYVIIA(B).
 OS Bacillus thuringiensis (subsp. dakota).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=132288;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA PAYNE J.M., Fu J.M.;
 RT "Coleopteran-active toxins";
 RL Patent number US5286486, 15-FEB-1994.
 CC -1- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
 CC EPITHELIAL CELLS OF COLEOPTERA.
 CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
 CC SPOULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART OF
 CC THE SPORE COAT.
 CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE N-
 CC TERMINUS.
 CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
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 CC modified and this statement is not removed. Usage by and for commercial
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 CC or send an email to license@isb-sib.ch).
 CC EMBL; U04367; AAA21120.1; .
 DR HSSP; P07130; IDLC.
 DR InterPro; IPR001178; Endotoxin.
 DR InterPro; IPR005638; endotoxin_C.
 DR InterPro; IPR005639; endotoxin_N.
 DR Pfam; PF00555; endotoxin_1.
 DR Pfam; PF03944; endotoxin_C_1.
 DR Pfam; PF03945; endotoxin_N_1.

KM Toxin; Sporulation.
 SQ SEQUENCE 1138 AA; 129778 MW; 01DF072C074CE88 CRC64;
 Query Match 9.2%; Score 306; DB 1; Length 1138;
 Best Local Similarity 20.0%; Pred. No. 7,3e-13;
 Matches 135; Conservative 109; Mismatches 22; Indels 208; Gaps 25;
 QY 52 PIVGVSFLKTKVSLIGKRLISELMGLIPFGSGTLMODILRETEPQLOMNTDTLA 111
 Db 76 PGASFITNFKL-----ITGLMFW-NKIMNEFEETVEITLQKIEQARN 121
 QY 112 RVNAHEEGIANIRENQVDNFIAPTONPVPLS-ITSSVNTMOQLFNRLPQRFVQGY 170
 Db 122 KALAELEGANNLTITYQALDEMLNPPDPATIRVIDREPRILDALFESYMPSEFVAGYE 181
 QY 171 LLLPLFAQANMHLSPFRDVNLNADWGISATLFTYQNYLKNYTRYSNVCINTQTA 230
 Db 182 IPLLTVYAQANLHLALRLDSTLYGDKMGFPQNNIEENTYRQKKHISYSHCVKWTNSG 241
 QY 231 FRGLNRLHDLN---EFTYMFANVFYVSIWGLFKYQSLVSGANLVASGSGPOQTQ 286
 Db 242 LSRINGSTYEQWINKYRFRREMLMVLDAVFIYD----- 278
 QY 287 SFTSQDMPFLYSILFQVNSNYVLNGFSGARLTQTFPNIGLPGTTTHALLARVNSGVY 346
 Db 279 -----PRMTSM-----ET-----STQLTRVYTDPISLIS--I 303
 QY 347 SSGDIGAVFNONFSCSTFLPLLPPLTPVASMID----- 378
 Db 304 SNPDIGFSPSQMENTA-----FRTPLVDYLDLBYLTYSKYAFSHEIQPDLFYWCYHKV 358
 QY 379 --SGSDRGVNTVNTMQTESFEFTLG-LRCAAFARAKNSNYPEDYFINISGVLVVRNE 435
 Db 359 SFFKSSQSLVLT---TGIVGTSGYISGASVFRNDIY---RTLAASVVV--- 404
 QY 436 DLRRPLHNEIRNIES--GTPGGLRAYVSVHNRKNNIY-----AYHE 478
 Db 405 ---YPTQYGVGEVYEVGVG---HAYRQDNKYLDLYDSIDQLPPDGEIHE 452
 QY 479 -----NGTMIHLAPEDYGTFTSPHATQVNNQGTTFISKFGNQGSLRFGSNTTA 531
 Db 453 KYTHRLCHATAISKSTPDYDNATI-PIFSW-----THSAEYNYRILYPRKIKKIPAVK 504
 QY 532 RYTL-----RG-NG-----NSNYLYLRVSSLGNTSTR 557
 Db 505 MYGLDLDLTVYKGGFTGSDYLRKSGNYIDIKATVNSPLSQKRYRVRVATSVSGLFN 564
 QY 558 VTINGRVYTAGSNVNTT--TNDGVNDNGARPLDINMGNVASDNTNVPLDINVT-FNSGT 614
 Db 565 VFINDIELALQKNFQSVTFETIGGKDLVYGSFYBYSTTIQPNHPRKTLHLNHLNNS 624
 QY 615 QFELNIMVEPTNL 628
 Db 625 PFYVDSIEPIFVDV 638
 RESULT 15
 ID C1BE BACTU STANDARD; PRT; 1227 AA.
 AC 085805:
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pesticidal crystal protein cryIbE (insecticidal delta-endotoxin
 DE CryIbE) (Crystalline entomocidal protoxin) (139 kDa crystal protein).
 GN CRYIbE OR CRYIb(E) OR 158C2B.
 OS Bacillus thuringiensis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1428;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRRL B-18872 / PS158C2;

us-10-040-906a-2.rsp

Page 12

CC -1- DEVELOPMENTAL STAGE: THE CRISTAL PROTEIN IS PRODUCED DURING
CC SPOULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
CC OF THE SPORE COAT.
CC
CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE

CC
DR EMBL, AF077326; AAC32850.1; -.
DR HSSP, P07130; IDLC.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR Pfam; PF00555; endotoxin_C; 1.
DR Pfam; PF03944; endotoxin_C; 1.
DR Pfam; PF03945; endotoxin_N; 1.
DR Toxin; Sporulation; Pfam5d.
SQ SSQUNCE 1227 AA; 135084 MW; CBAB7BEA0B34CD3 CRC64;

Query Match	9.2%	Score 305.5;	DB 1;	Length 1227;
Best Local Similarity	22.5%;	Pred. No. 8.8e-13;		
Matches 142;	Conservative 101;	Mismatches 265;	Indels 123;	Gaps 25;

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OY      52  PIVATVSPFLKVKVSLGRILRLESEMOJLPPSGSNTIMOOJLEFEQCLANRANTTLLA 111
Db      73  PFAQJLASYSFLVG-----ELM-----PFG-RDPEIFLEHVEQJLRQQTENTRD 118
OY      112  RVNMELEGLQANIEFNOQVDNFIAMPONPVLSTISSVNTMOOL-FIKRLPQRRVGYO 170
Db      119  TALARKQJGNSFRFYQOQSLDEMLERDARTASVLYTQJYALDPLDIAMLPLPFIINQO 178
OY      171  LLLPLPFAQAMMHLSPFRDVVLNADDEWGISATLTYQNYLKNVITYESNYCINTYQTA 230
Db      179  VPLIMVYAQAAMHLLILRLDASJFCGSEGLTSGOIRORYERQVETAEYSDYCARWNTG 238
OY      231  FRGI-NTRLHDL---BFRYTMFLWPEYVSIMSLPKOYSLTSSGANT---VASGSG 282
Db      239  LNNIRGTMASMLRKNQFRDRLTGLVDVVALPFSYDTRVYPMNTSMLTIREIYDPIGR 298
OY      283  OQOTOS-FTSGDWPFLYSLFQVNSNYLWNGSGLARLQTR-PRIGLPGTTTHALLAAR 340
Db      299  TNAPSGASTNM-----FNNN-APSFALBAAVIRPRLDDEPQULTFVSLSRMS 348
OY      341  NYSGVSGSDIGAVENQNFSCSTPLPPLTPEFVSW---LDSGSDRGCAWTVN----- 391
Db      349  N-----TQYMWVGHRLSERTTIGSLSTSHGWNTR 380
OY      392  -----WQTESPES-----TLGIRGCAATLRGNSNPFDPYIRNI--SG 427
Db      381  SINPVLQFTSRDQVRLTSPAGINILLTTPVNPGAPARAKWNRKMLNSKGLSLITIGTG 440
OY      428  VPLVVRNEDLRRLHYNIEINRIESPSPGFGGLRAYVSVHNRKNNIYA-VHENGTMILHA 486
Db      441  VGTOLFSETELPETTERPRVYESVHRLSNIR--LISGNTLRPARYSWTHASA----- 492
OY      487  PEDYGTGTISPLHAROVN-----NQRTRISPKKNGOGSLPFEOSWTRAYLRKNG 539
Db      493  --DRTN-TLSSDSITQIDLYKXSFNLNSGTVSSDPGFGDIINTNNNSGLSWGLAPNN 549
OY      540  NS---YMLIRVSSIGSNSTRVITNG-RVYIASVNTTNNNDGVNDGARFLDIMGNV 555

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Db 550 TSIQRKRRVRRVYAAAGQMILRLRTVGGSTPDPQGFPESTVSNANESULTSGSPFAALFPVYGISA 603

QY 596 ASDNTNVPDLINTVFNSSGTO-FELANNINFPV 625

Db 610 SSGSOT--AGISISNAGRGQTFHPDKLRFP 637

Search completed: August 14, 2003, 18:11:15
Job time : 17 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 14, 2003, 18:08:52 ; Search time 46 Seconds

(without alignments)
3545.418 Million cell updates/sec

Title: US-10-040-906A-2

Perfect score: 3314

Sequence: 1 MNVNLNGRTTICDAVNVVA.....GTQELMNMVFNLEPPIY 632

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SP_ARCHA:.*
2: SP_BACTERIA:.*
3: SP_FUNGI:.*
4: SP_HUMAN:.*
5: SP_INVERTEBRATE:.*
6: SP_MAMMAL:.*
7: SP_MHC:.*
8: SP_ORGANELLE:.*
9: SP_PHAGE:.*
10: SP_PLANT:.*
11: SP RODENT:.*
12: SP_VIRUS:.*
13: SP_VERTEBRATE:.*
14: SP_UNCLASSIFIED:.*
15: SP_IVIRUS:.*
16: SP_BACTERIAP:.*
17: SP_ARCHAEP:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3044.5	91.9	633	2 Q8GHF3	Q8GHF3 bacillus th
2	3029.5	91.4	633	2 Q9S6N5	Q9S6N5 bacillus th
3	3025.5	91.3	633	2 Q9S6N4	Q9S6N4 bacillus th
4	2998.5	90.5	633	2 Q8GH90	Q8GH90 bacillus th
5	2641.5	79.7	551	2 Q8RM99	Q8RM99 bacillus th
6	328.5	9.9	1231	2 Q8RM92	Q8RM92 bacillus th
7	327.5	9.9	719	2 Q93N15	Q93N15 bacillus th
8	325.5	9.8	719	2 Q83N15	Q83N15 bacillus th
9	323.5	9.8	719	2 Q83N15	Q83N15 bacillus th
10	317.5	9.6	719	2 Q83N15	Q83N15 bacillus th
11	280.5	8.5	1180	2 Q9S5V8	Q9S5V8 bacillus th
12	279.5	8.4	645	2 Q9S603	Q9S603 bacillus th
13	278.5	8.4	1228	2 Q93NMS	Q93NMS bacillus th
14	277.5	8.3	381	2 Q45740	Q45740 bacillus th
15	276.5	8.3	620	2 Q45720	Q45720 bacillus th
16	276.5	8.3	1176	2 Q45736	Q45736 bacillus th

17	276.5	8.3	1228	2 Q93T75	Q93T75 bacillus th
18	274.5	8.2	1176	2 Q9S514	Q9S514 bacillus th
19	270.5	8.2	1118	2 Q9AM83	Q9AM83 bacillus th
20	270.5	8.2	1176	2 Q9RC30	Q9RC30 bacillus th
21	270	8.1	1177	2 Q8GLY5	Q8GLY5 bacillus th
22	268	8.1	1155	2 Q9P296	Q9P296 bacillus th
23	264.5	8.0	1178	2 Q9P826	Q9P826 bacillus th
24	264	8.0	723	2 Q9S4B5	Q9S4B5 bacillus th
25	264	8.0	1174	2 Q45749	Q45749 bacillus th
26	264	8.0	1177	2 Q03743	Q03743 bacillus th
27	263	7.9	1155	2 Q93T21	Q93T21 bacillus th
28	262.5	7.9	1144	2 Q8KZL7	Q8KZL7 bacillus th
29	262	7.9	638	2 Q87654	Q87654 bacillus th
30	261.5	7.9	1178	2 Q45768	Q45768 bacillus th
31	259	7.8	1177	2 Q45735	Q45735 bacillus th
32	257.5	7.8	1236	2 Q939T3	Q939T3 bacillus th
33	255.5	7.7	618	2 Q32306	Q32306 bacillus th
34	255	7.7	1118	2 Q9AM82	Q9AM82 bacillus th
35	253	7.6	607	2 Q45721	Q45721 bacillus th
36	253	7.6	618	2 Q45737	Q45737 bacillus th
37	250	7.5	652	2 Q9S6N9	Q9S6N9 bacillus th
38	246	7.4	1169	2 Q8GH88	Q8GH88 bacillus th
39	244	7.4	1160	2 Q93TF9	Q93TF9 bacillus th
40	237	7.2	650	2 Q8VNX2	Q8VNX2 bacillus th
41	231.5	7.0	1189	2 Q91877	Q91877 bacillus th
42	230	6.9	7.0	2 Q8ROU6	Q8ROU6 bacillus th
43	226	6.5	1144	2 Q45745	Q45745 bacillus th
44	214.5	6.5	1171	2 Q06894	Q06894 bacillus th
45	212	6.4	723	2 Q9EV82	Q9EV82 bacillus th

ALIGNMENTS

RESULT 1

Q8GHF3 PRELIMINARY: PRT; 633 AA.
AC Q8GHF3; 01-MAR-2003 (TREMURel. 23, Created)
DT 01-MAR-2003 (TREMURel. 23, Last sequence update)
DT 01-MAR-2003 (TREMURel. 23, Last annotation update)
DE Insecticidal crystal protein Cry2Aa.
GN CRY2Aa.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OK NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Dongbei 66;
RA Wei G., Jie Z., Dafang H., Guoxun L.;
RT "New cry2Aa gene from Chinese native isolates Bt strain Dongbei 66.";
RL Submitted (ABR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF252262; AMO13734.1; -
SQ SEQUENCE 633 AA; 70822 MW; 9CA19991B78798A6 CRC64;

Query Match 91.9%; Score 3044.5; DB 2; Length 633;
Best Local Similarity 90.5%; Pred. No. 1e-196;
Matches 573; Conservative 34; Mismatches 25; Indels 1; Gaps 1;

Qy	1	MNVNLNGRTTICDAVNVVAADPPSEFHSKLTTRKEMWETDHSIYAVIGVYSSP	60
Db	1	MNVNLNGRTTICDAVNVVAADPPSEFHSKLTTRKEMWETDHSIYAVIGVYSSP	60
Qy	61	LKKVGSGLGRIILSELWGLIFPSGSTNLMODILRETEQFLNRLNTDTLARNVAEGL	120
Db	61	LKKVGSGLGRIILSELWGLIFPSGSTNLMODILRETEQFLNRLNTDTLARNVAEGL	120
Qy	121	QANIRENOOVNPNPNQNPVPLSTSSVTMTQQLPLNLPFRQYQYQILLPLFQA	180
Db	121	QANIRENOOVNPNPNQNPVPLSTSSVTMTQQLPLNLPFRQYQYQILLPLFQA	180
Qy	181	ANHEISFIDVVLNADWEGISAATLRTYQNYLKNYTTESGNYINTYQATRGATRLHD	240
Db	181	ANHEISFIDVVLNADWEGISAATLRTYQNYLKNYTTESGNYINTYQATRGATRLHD	240

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Db      181 ANHLSFIRDVILNADENKISAAATLRTYRDYLRNVTBDSNYCINTYQTAFRGLNTRLHD 240
Qy      241 MLEFRTYFLNVEEYVSIWLSLFKQSLVSSGANLYASGSGPOQTOSFTSQDMPFLYSLF 300
Db      241 MLEFRTYFLNVEEYVSIWLSLFKQSLVSSGANLYASGSGPOQTOSFTSQDMPFLYSLF 300
Qy      301 QVNSNYVLNGFSGARLJOTFPNIGGLPGTTTHALLAARVNSGVSSGSDIGAV-FNOMF 359
Db      301 QVNSNYVLNGFSGARLJOTFPNIGGLPGTTTHALLAARVNSGVSSGSDIGAV-FNOMF 360
Qy      360 SCSTFLPPLLPFRVMSLDSGDRGVNTVMQTESPESTGLRCGAFARAGNSYFPD 419
Db      361 NCSTVLPPLSTPFVMSLDSGDRGVNTVMQTESPESTGLRCGAFARAGNSYFPD 420
Qy      420 YFIRNISGVPLVRNEDLRPLAHNEIRNIESPSGTPGGLRAYVSVHNRKNNTYAVHEN 479
Db      421 YFIRNISGVPLVRNEDLRPLAHNEIRNIESPSGTPGGLRAYVSVHNRKNNTYAVHEN 480
Qy      480 GTMHLAPEDYTGFTISPIHATQVNNQRTFISEKFGQDGLRFGOSNTTARTYLRGNG 539
Db      481 GTMHLAPEDYTGFTISPIHATQVNNQRTFISEKFGQDGLRFGOSNTTARTYLRGNG 540
Qy      540 NSYNLYRVSLSGNSITIRVTINGRVTYASNVTTTNDGVNDGARFLDINMGVVASDN 599
Db      541 NSYNLYRVSLSGNSITIRVTINGRVTYASNVTTTNDGVNDGARFLDINMGVVASDN 600
Qy      600 TNPVLDINTFNSGTOPELNMIMFPTNLPPIY 632
Db      601 TNPVLDINTFNSGTOPELNMIMFPTNLPPIY 633

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RESULT 2

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ID      09S6N5      PRELIMINARY;      PRT;      633 AA.
AC      09S6N5;
DT      01-MAY-2000 (TREMBlrel. 13, Created)
DT      01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT      01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE      cry2Aa protein.
GN      CRY2Aa6.
OS      Bacillus thuringiensis.
OC      Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX      NCBI_TaxID=1428;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=Y271;
RA      Yu J., Pang Y.;
RT      "Cloning and characterisation of insecticidal crystal protein gene
RT      cry2Aa6 from new isolated strain of Bacillus thuringiensis Y271.";
RL      Submitted (FEB-1999) to the EMBL/Genbank/DBJ databases.
RL      EMBL: AJ132465; CA10672.1; -
DR      InterPro: IPR005638; endotoxin_C.
DR      InterPro: IPR005639; endotoxin_N.
DR      Pfam: PF03944; endotoxin_C; 1.
DR      Pfam: PF03945; endotoxin_N; 1.
SQ      SEQUENCE 633 AA; 70837 MW; CC727E33B75A583 CRC64;

```

Query Match

91.4%; Score 3029.5; DB 2; Length 633;
 Best Local Similarity 90.0%; Pred. No. 1.e-195;
 Matches 570; Conservative 36; Mismatches 26; Indels 1; Gaps 1;

```

Qy      1 MNNVLANGRTTICDAVNVVAHDPFSFEKSLDITRKEMEMKRTDHSLYVAPVIGTVSSF 60
Db      1 MNNVLANGRTTICDAVNVVAHDPFSFEKSLDITRKEMEMKRTDHSLYVAPVIGTVSSF 60
Qy      61 LKKVGSILGKRIISLWGLIFPSSGNTLMODILRETEQFLNQRLNTDTLARVNAIEGL 120
Db      61 LKKVGSILGKRIISLWGLIFPSSGNTLMODILRETEQFLNQRLNTDTLARVNAIEGL 120
Qy      121 QANIREFNOVDNPLNPTONPVPLSTSSVNTMQCLFLNRLPQFQIGYQLLLPLFAQA 180
Db      121 QANIREFNOVDNPLNPTONPVPLSTSSVNTMQCLFLNRLPQFQIGYQLLLPLFAQA 180

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Qy      181 ANHLSFIRDVILNADENKISAAATLRTYRDYLRNVTBDSNYCINTYQTAFRGLNTRLHD 240
Db      181 ANHLSFIRDVILNADENKISAAATLRTYRDYLRNVTBDSNYCINTYQTAFRGLNTRLHD 240
Qy      241 MLEFRTYFLNVEEYVSIWLSLFKQSLVSSGANLYASGSGPOQTOSFTSQDMPFLYSLF 300
Db      241 MLEFRTYFLNVEEYVSIWLSLFKQSLVSSGANLYASGSGPOQTOSFTSQDMPFLYSLF 300
Qy      301 QVNSNYVLNGFSGARLJOTFPNIGGLPGTTTHALLAARVNSGVSSGSDIGAV-FNOMF 359
Db      301 QVNSNYVLNGFSGARLJOTFPNIGGLPGTTTHALLAARVNSGVSSGSDIGAV-FNOMF 360
Qy      360 SCSTFLPPLLPFRVMSLDSGDRGVNTVMQTESPESTGLRCGAFARAGNSYFPD 419
Db      361 NCSTVLPPLSTPFVMSLDSGDRGVNTVMQTESPESTGLRCGAFARAGNSYFPD 420
Qy      420 YFIRNISGVPLVRNEDLRPLAHNEIRNIESPSGTPGGLRAYVSVHNRKNNTYAVHEN 479
Db      421 YFIRNISGVPLVRNEDLRPLAHNEIRNIESPSGTPGGLRAYVSVHNRKNNTYAVHEN 480
Qy      480 GTMHLAPEDYTGFTISPIHATQVNNQRTFISEKFGQDGLRFGOSNTTARTYLRGNG 539
Db      481 GTMHLAPEDYTGFTISPIHATQVNNQRTFISEKFGQDGLRFGOSNTTARTYLRGNG 540
Qy      540 NSYNLYRVSLSGNSITIRVTINGRVTYASNVTTTNDGVNDGARFLDINMGVVASDN 599
Db      541 NSYNLYRVSLSGNSITIRVTINGRVTYASNVTTTNDGVNDGARFLDINMGVVASDN 600
Qy      600 TNPVLDINTFNSGTOPELNMIMFPTNLPPIY 632
Db      601 TNPVLDINTFNSGTOPELNMIMFPTNLPPIY 633

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RESULT 3

```

ID      09S6N4      PRELIMINARY;      PRT;      633 AA.
AC      09S6N4;
DT      01-MAY-2000 (TREMBlrel. 13, Created)
DT      01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT      01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE      cry2Aa protein.
GN      CRY2Aa5.
OS      Bacillus thuringiensis.
OC      Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX      NCBI_TaxID=1428;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=SL39;
RA      Yu J., Pang Y.;
RT      "Cloning and characterisation of insecticidal crystal protein gene
RT      cry2Aa5 from new isolated strain of Bacillus thuringiensis SL39.";
RL      Submitted (FEB-1999) to the EMBL/Genbank/DBJ databases.
RL      EMBL: AJ132464; CA10671.1; -
DR      InterPro: IPR005638; endotoxin_C.
DR      InterPro: IPR005639; endotoxin_N.
DR      Pfam: PF03944; endotoxin_C; 1.
DR      Pfam: PF03945; endotoxin_N; 1.
SQ      SEQUENCE 633 AA; 70925 MW; 8FB7F5216AC67B8 CRC64;

```

Query Match

91.3%; Score 3025.5; DB 2; Length 633;
 Best Local Similarity 90.0%; Pred. No. 2e-195;
 Matches 570; Conservative 35; Mismatches 27; Indels 1; Gaps 1;

```

Qy      1 MNNVLANGRTTICDAVNVVAHDPFSFEKSLDITRKEMEMKRTDHSLYVAPVIGTVSSF 60
Db      1 MNNVLANGRTTICDAVNVVAHDPFSFEKSLDITRKEMEMKRTDHSLYVAPVIGTVSSF 60
Qy      61 LKKVGSILGKRIISLWGLIFPSSGNTLMODILRETEQFLNQRLNTDTLARVNAIEGL 120
Db      61 LKKVGSILGKRIISLWGLIFPSSGNTLMODILRETEQFLNQRLNTDTLARVNAIEGL 120
Qy      121 QANIREFNOVDNPLNPTONPVPLSTSSVNTMQCLFLNRLPQFQIGYQLLLPLFAQA 180
Db      121 QANIREFNOVDNPLNPTONPVPLSTSSVNTMQCLFLNRLPQFQIGYQLLLPLFAQA 180

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Db      121 QANIREFNOQVNFNLPONPVLSTSSVNTMOQLFLNRLPQFOIGYQLLLPLFAQA 180
Qy      181 AMHLSFTRDVVNLNADENGISATLRTYQVNLKNTTEYSNCINTYQTAFRGLNTRLHD 240
Db      181 AMHLSFTRDVVNLNADENGISATLRTYQVNLKNTTEYSNCINTYQTAFRGLNTRLHD 240
Qy      241 MLEFRTYMEFLANFEYYSIWSLFFKQSLIVSSGANLYASGGSPQOOTSFOISQDMPFLYSLF 300
Db      241 MLEFRTYMEFLANFEYYSIWSLFFKQSLIVSSGANLYASGGSPQOOTSFOISQDMPFLYSLF 300
Qy      301 QVNSNYVLNGFSGALNLTOTFPNIGLPGTTTHALLAARVYSGVSGSDIGA-VERQNF 359
Db      301 QVNSNYVLNGFSGALNLTOTFPNIGLPGTTTHALLAARVYSGVSGSDIGA-VERQNF 359
Qy      360 SCSTFPLPPLTFPVRSWLDGSDRGVNTVMQTESFESTLGLRCGAFTRAGNSNFPD 419
Db      360 SCSTFPLPPLTFPVRSWLDGSDRGVNTVMQTESFESTLGLRCGAFTRAGNSNFPD 419
Qy      420 YFIRNISGVLVVRNEDLRPLHYNEIRNISPSGTCGGLRAVMSVHNRKNITVAHEN 479
Db      420 YFIRNISGVLVVRNEDLRPLHYNEIRNISPSGTCGGLRAVMSVHNRKNITVAHEN 479
Qy      480 GTMHLAPEDYTGFTISPIHATOVNNOQTRFISEKFGNQSDSLRFEQNTTARATLRKNG 539
Db      480 GTMHLAPEDYTGFTISPIHATOVNNOQTRFISEKFGNQSDSLRFEQNTTARATLRKNG 539
Qy      540 NSNYLYLRVSSIGNSTIRVTINGRYTASNNVTNNNDGVNDGARFSDINIGVYASSN 599
Db      540 NSNYLYLRVSSIGNSTIRVTINGRYTASNNVTNNNDGVNDGARFSDINIGVYASSN 599
Qy      600 TNPVLDINTVNSGTQPELMNIMFVPTNLPLPY 632
Db      601 TNPVLDINTVNSGTQPELMNIMFVPTNLPLPY 632

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RESULT 4

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ID      08GH90      PRELIMINARY;      PRT;      633 AA.
AC      08GH90;
DT      01-MAR-2003 (T-EMBLrel. 23, Created)
DT      01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
DT      01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE      Crystal delta-endotoxin.
GN      CRY2AB.
OS      Bacillus thuringiensis.
OC      Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX      NCBI_TaxID=1428;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=B-Pr-88;
RA      Li C., Zhang J., Huang D., Li G.;
RT      Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AF361115; AAO13296.1; -.
SQ      SEQUENCE 633 AA; 70726 MW; 01EFA3A35564D01 CRC64;

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Query Match 90.5%; Score 2998.5; DB 2; Length 633;

Best Local Similarity 89.4%; Pred. No. 1.3e-193; Indels 1; Gaps 1;

Matches 566; Conservative 40; Mismatches 26; Indels 1; Gaps 1;

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Qy      1 MNNVNLNGRTTICDAYNVVAHDPSPFEHKSIDTIRKEMWKRTHSLYVAVIVGVSSF 60
Db      1 MNNVNLNGRTTICDAYNVVAHDPSPFEHKSIDTIRKEMWKRTHSLYVAVIVGVSSF 60
Qy      61 LKLVGSLIGKRIISELWGLIFPGSGTNLMODILRETEQFNLORNTDPLAARNAELSEL 120
Db      61 LKLVGSLIGKRIISELWGLIFPGSGTNLMODILRETEQFNLORNTDPLAARNAELSEL 120
Qy      121 QANIREFNOQVNFNLPONPVLSTSSVNTMOQLFLNRLPQFOIGYQLLLPLFAQA 180
Db      121 QANIREFNOQVNFNLPONPVLSTSSVNTMOQLFLNRLPQFOIGYQLLLPLFAQA 180
Qy      181 AMHLSFTRDVVNLNADENGISATLRTYQVNLKNTTEYSNCINTYQTAFRGLNTRLHD 240

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Db      181 AMHLSFTRDVVNLNADENGISATLRTYQVNLKNTTEYSNCINTYQTAFRGLNTRLHD 240
Qy      241 MLEFRTYMEFLANFEYYSIWSLFFKQSLIVSSGANLYASGGSPQOOTSFOISQDMPFLYSLF 300
Db      241 MLEFRTYMEFLANFEYYSIWSLFFKQSLIVSSGANLYASGGSPQOOTSFOISQDMPFLYSLF 300
Qy      301 QVNSNYVLNGFSGALNLTOTFPNIGLPGTTTHALLAARVYSGVSGSDIGA-VERQNF 359
Db      301 QVNSNYVLNGFSGALNLTOTFPNIGLPGTTTHALLAARVYSGVSGSDIGA-VERQNF 359
Qy      360 SCSTFPLPPLTFPVRSWLDGSDRGVNTVMQTESFESTLGLRCGAFTRAGNSNFPD 419
Db      360 SCSTFPLPPLTFPVRSWLDGSDRGVNTVMQTESFESTLGLRCGAFTRAGNSNFPD 419
Qy      420 YFIRNISGVLVVRNEDLRPLHYNEIRNISPSGTCGGLRAVMSVHNRKNITVAHEN 479
Db      420 YFIRNISGVLVVRNEDLRPLHYNEIRNISPSGTCGGLRAVMSVHNRKNITVAHEN 479
Qy      480 GTMHLAPEDYTGFTISPIHATOVNNOQTRFISEKFGNQSDSLRFEQNTTARATLRKNG 539
Db      480 GTMHLAPEDYTGFTISPIHATOVNNOQTRFISEKFGNQSDSLRFEQNTTARATLRKNG 539
Qy      540 NSNYLYLRVSSIGNSTIRVTINGRYTASNNVTNNNDGVNDGARFSDINIGVYASSN 599
Db      540 NSNYLYLRVSSIGNSTIRVTINGRYTASNNVTNNNDGVNDGARFSDINIGVYASSN 599
Qy      600 TNPVLDINTVNSGTQPELMNIMFVPTNLPLPY 632
Db      601 TNPVLDINTVNSGTQPELMNIMFVPTNLPLPY 632

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RESULT 5

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ID      09RM89      PRELIMINARY;      PRT;      551 AA.
AC      09RM89;
DT      01-MAY-2000 (T-EMBLrel. 13, Created)
DT      01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT      01-OCT-2002 (T-EMBLrel. 22, Last annotation update)
DE      Cry2A protein (Fragment).
GN      CRY2AD.
OS      Bacillus thuringiensis.
OC      Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX      NCBI_TaxID=1428;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=Cy23;
RA      Yu J., Pang Y.;
RT      "Cloning and characterization of insecticidal crystal protein gene
RT      cry2ad from new isolated strain of Bacillus thuringiensis Cy23."
RT      Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AJ132463; CAA10670.2; -.
DR      InterPro; IPR005639; endotoxin_N.
DR      Pfam; PF03945; endotoxin_N; 1.
FT      NON_TER 551
SQ      SEQUENCE 551 AA; 62126 MW; D6B77B8AET713B98A CRC64;

```

Query Match 79.7%; Score 2641.5; DB 2; Length 551;

Best Local Similarity 90.4%; Pred. No. 1.2e-163; Indels 1; Gaps 1;

Matches 498; Conservative 30; Mismatches 22; Indels 1; Gaps 1;

```

Qy      1 MNNVNLNGRTTICDAYNVVAHDPSPFEHKSIDTIRKEMWKRTHSLYVAVIVGVSSF 60
Db      1 MNNVNLNGRTTICDAYNVVAHDPSPFEHKSIDTIRKEMWKRTHSLYVAVIVGVSSF 60
Qy      61 LKLVGSLIGKRIISELWGLIFPGSGTNLMODILRETEQFNLORNTDPLAARNAELSEL 120
Db      61 LKLVGSLIGKRIISELWGLIFPGSGTNLMODILRETEQFNLORNTDPLAARNAELSEL 120
Qy      121 QANIREFNOQVNFNLPONPVLSTSSVNTMOQLFLNRLPQFOIGYQLLLPLFAQA 180
Db      121 QANIREFNOQVNFNLPONPVLSTSSVNTMOQLFLNRLPQFOIGYQLLLPLFAQA 180

```

QY 181 ANHLSFRDVLNADENGISAATLTQNYLAKNTTETRYNCINTYQTPARGANTRELD 240
 DB 181 ANHLSFRDVLNADENGISAATLTQNYLAKNTTETRYNCINTYQTPARGANTRELD 240
 QY 241 MLBERTMFLANFEVYSIWSLFKYOSLIVSAGANLYASGSGPOOTOSPTSDPPELYSLF 300
 DB 241 MLBERTMFLANFEVYSIWSLFKYOSLIVSAGANLYASGSGPOOTOSPTSDPPELYSLF 300
 QY 301 QVNSNYVLNFGSGANLTOTFPNIGLPGTTTHALLARVNSGVSQSDIGAV-PN0NF 359
 DB 301 QVNSNYVLNFGSGANLTOTFPNIGLPGTTTHALLARVNSGVSQSDIGAV-PN0NF 359
 QY 301 QVNSNYVLNFGSGANLTOTFPNIGLPGTTTHALLARVNSGVSQSDIGAV-PN0NF 359
 DB 301 QVNSNYVLNFGSGANLTOTFPNIGLPGTTTHALLARVNSGVSQSDIGAV-PN0NF 359
 QY 360 SCSTFLPPLTTPFVSWLDSGDRGVNVTVMQTESPESTLGRCAFTAGNSNFPD 419
 DB 360 SCSTFLPPLTTPFVSWLDSGDRGVNVTVMQTESPESTLGRCAFTAGNSNFPD 419
 QY 361 NCSYVLPPLSTPFVSWLDSGDRGVNVTVMQTESPESTLGRCAFTAGNSNFPD 420
 DB 361 NCSYVLPPLSTPFVSWLDSGDRGVNVTVMQTESPESTLGRCAFTAGNSNFPD 420
 QY 420 YFINISGVPLVVRNEDLRPLHAYNEIRNIESPSGTPGALAYVNSVHRKKNIYAHEN 479
 DB 420 YFINISGVPLVVRNEDLRPLHAYNEIRNIESPSGTPGALAYVNSVHRKKNIYAHEN 479
 QY 421 YFINISGVPLVVRNEDLRPLHAYNEIRNIESPSGTPGALAYVNSVHRKKNIYAHEN 480
 DB 421 YFINISGVPLVVRNEDLRPLHAYNEIRNIESPSGTPGALAYVNSVHRKKNIYAHEN 480
 QY 480 GTMHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNGDGLFEQSNTPATYLRNG 539
 DB 480 GTMHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNGDGLFEQSNTPATYLRNG 539
 QY 481 GTMHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNGDGLFEQSNTPATYLRNG 540
 DB 481 GTMHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNGDGLFEQSNTPATYLRNG 540
 QY 540 NSYNLYRVSS 550
 DB 540 NSYNLYRVSS 551

RESULT 6

ID Q8KNY2 PRELIMINARY; PRT; 1231 AA.

AC Q8KNY2; 01-OCT-2002 (TREMblrel. 22, Created)
 DT 01-OCT-2002 (TREMblrel. 22, Last sequence update)
 DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
 DE CRY1B1.
 GN CRY1B1.
 OS Bacillus thuringiensis.
 CC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 NCBI_TaxId=1428;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=834;
 RA Isakova I.A., Isakov Y.B., Ryamar' S.E., Yarovoi S.V.,
 RT "Cloning of a novel Bacillus thuringiensis cry1B1 gene for
 insecticidal crystal protein."
 RL Submitted (Aug-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY138457; AAM93496.1; -;
 DR InterPro: IPR001178; Endotoxin.
 DR InterPro: IPR005639; endotoxin_C.
 DR InterPro: IPR005639; endotoxin_N.
 DR Pfam: PF03944; endotoxin_C; 1.
 DR Pfam: PF03945; endotoxin_N; 1.
 DR Pfam: PF03945; endotoxin_N; 1.
 SQ SEQUENCE 1231 AA; 139765 MW; C9F2848A9297EA00 CRC64;

Query Match

Best Local Similarity 23.3%; Pred. No. 2, 1e-13; Matches 155; Conservative 101; Mismatches 249; Indels 161; Gaps 29;

QY 52 PIVGVTSFLKKVGLIGKRILISELWGLIFPSSGSTMMDILRETEQFLNORLNTDTLA 111
 DB 73 PFAQGLASFSFLVY-----ELM-----PSG-RDPWEIFLEHVEQLIQVNTENTN 118
 QY 112 RVNAELGQANIRENQOVNPIANPTQNPVPLSITSVNTMQL-FINRLPQFVQVQ 170
 DB 119 TAIARLEGGRGYSYQALLETWLDNRNARSRIILERYVALDELDTTALPLRIRNEE 178
 QY 171 LLLPLPFAQANHLISFRDVLNADENGISAATLTQNYLAKNTTETRYNCINTYQTA 230
 DB 179 VPLIMVYQAQANLHLLLRDASLFGSEWGMASDVNOYQOIRYTBESNHCVMYNTG 238

QY 231 FGL-NTLHML-EPFTYFLNVEEYYSIWSLFKYOSLIVSAGANL---YASGSG 282
 DB 239 LNNLGTASQMLRYNQFRDLTLGLDLVALPSPYDTETPIYISQLRLREITDPIGR 298
 QY 283 QQTQS-FTSQW-----PFLSYLQVNSNY----LNGFSG 313
 DB 299 TNAPSGFASIMVENNNAAPSALIAAIRPHLLDPEDGLITISASBRMSSTQHMYWVG 358
 QY 314 ARLTQFPNIGLPGTTTHALLARVNSGVSQSDIGAVNQNFCSTFLPPLTPPV 373
 DB 359 HRL--NFRPIGLMTST-----QGLTNVSYINPVLQFT 391
 QY 374 RSWLDSGDRGVN---TVTN---WQTESPESTLGRCAFTAGNSNFPYFIRNIS 426
 DB 392 SDVYRTESNAGNLTFTTPVNGVWDFNFINQNI-----YEGATYSGPY-----Q 441
 QY 427 GVEPLVRNEDLRPLHAYNEIRNIESPS-----GTPEG--LAAYVS-VH----- 467
 DB 442 GVGIGLQFSETELEPPETTERPNYESHRLSHIGLIGTLAPAPYSWTHRSADRNTTIG 501
 QY 468 -NRKNIYAYHE---NGTWHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNGDGL 522
 DB 502 PNRIQIPAYKGRFLRGSVI--SGPGFTGDVYRLNRNNGNIQNRGYI-----EV 550
 QY 523 RFQSNTPATYLRNGSNYNLYRVSSIGNSTRTVY-NGRVTAPASVNTTNDGVND 581
 DB 551 PIQFTSTSTRYVR-----VRYASTSIEELNVLGSSIFNTIIPATASLNDQS 601
 QY 582 NGARFLDIN-----MGNVVA-----SDYTNVPLD-----INVTFNSGTQFEL-----MNI 621
 DB 602 GDFGYEINNAFTSAGNIYAGNPFANAWEYIDRFEFIPVTEAREADYDLERAQKAYNA 661
 QY 622 MEVPNT 627
 DB 662 LFTSTN 667

RESULT 7

ID Q9JN5 PRELIMINARY; PRT; 719 AA.

AC Q9JN5; 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
 DT 01-OCT-2002 (TREMblrel. 22, Last annotation update)
 DE CRY1A.
 GN CRY1A.
 OS Bacillus thuringiensis.
 CC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 NCBI_TaxId=1428;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Song F., Zhang J., Gu A., Huang D., Li G.,
 RT "A novel Cry1A endotoxin."
 RL Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF373207; AAK66742.1; -;
 DR InterPro: IPR001178; Endotoxin.
 DR InterPro: IPR005639; endotoxin_C.
 DR InterPro: IPR005639; endotoxin_N.
 DR Pfam: PF00555; endotoxin_C; 1.
 DR Pfam: PF03944; endotoxin_C; 1.
 DR Pfam: PF03945; endotoxin_N; 1.
 DR Pfam: PF03945; endotoxin_N; 1.
 SQ SEQUENCE 719 AA; 81225 MW; C629DF2C44827241 CRC64;

Query Match

Best Local Similarity 22.8%; Pred. No. 1, 1e-13; Matches 162; Conservative 103; Mismatches 271; Indels 173; Gaps 32;

QY 21 HDPSEFEK---SLTTRKEM-MEMKRTD-----SLY--VAP----- 52
 DB 9 HOSFSSNAKYDKISTSLKNETDIEONINHEDCMLSEIENVEPFPYASATIGTGIGIAG 68
 QY 53 -IVGVSSFLKKVGLIGKRILISELWGLIFPSSGSTMMDILRETEQFLNORLNTDTLA 111
 DB 53 -IVGVSSFLKKVGLIGKRILISELWGLIFPSSGSTMMDILRETEQFLNORLNTDTLA 111

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Db      69 KILGTLGVPPAGQVSLY-SFILGELM-----PKGK-NQMEIFMEHVEEIIINQKISTYARN 122
Qy      112 RVNALEGLQANIRENQOVDFINPTQNPVLSIT-SSVNTMOQLFNLPPFRVQGY 170
Db      123 KALTDKLGIDALAVYHDSLESWGNRRASVAKSYIALBELMFOKLSFAVSGEE 182
Qy      171 LLLPLPFOAANMLSPFRDVLVLADEWGISAAATLRTYQNTLKNYTESNYCINTYQTA 230
Db      183 VPLPPIYAOANLHLMLLDASIFGKEWGLSSSEISTFYNQOVERADYSDHCWKVYSTG 242
Qy      231 FRGL-NTRLHML--EFTYVFLNVEYVSIWLSFKYOSLIVSSGANL-----YASGSGP 282
Db      243 LNNLRGTNAESWVRVYQFRDMLTMDLVALPSPYDQMPITKTAQLTREYTDALGT 302
Qy      283 QQTQ-SFTSQDW-----PFL-----YSLPQVNSN-YVINGFSG 313
Db      303 VHPHSFTSTTWNANNAPEFSAIEAAVVRNPHLDLFLQVITYSLSRMSNTQYMMWMC3 362
Qy      314 ARLQTPPNIGLPGTTTHALLAARVNVSGVSGDIGAVFNQFSCSTPLPPLTPPV 373
Db      363 HKL--EFTTIGTLINIST-----QGSTNTSINPVLTPFT 394
Qy      374 RSWLDSGSDRGVNVTV-----NMQ--TESPESTLGLRCGAFTRAGNSYPPD 419
Db      395 SRDVRTESLAGNLPLTPQVNGVRVDPHKVFTHPIAS-----DNFYYPG 441
Qy      420 YFIRNISGVPLVVRNEDLRPLHNEIRNIESPGTGGRLAAYVSVHNRKNNTIYA-VHE 478
Db      442 Y-----AGIGTQLODSENELPPEATQPNYESYSHLSHG-LISASHKALVYSWTHR 494
Qy      479 NGTMHLAPEDYGTFTISPIHATQV-----NQRTTFISEKFG-NQGSRLREGSNTTA 531
Db      495 SA-----DRTN-TIEPNSITQIPLVKAFLSSGAAYVGRGFTGDIIR-RITVGT 543
Qy      532 RYTLRNGN-----SYNLRYVSLNSSTIRVTINGRYTASVNTTTNDGVNDGARF 586
Db      544 FGDIRVNIKPPAQRVIRVASTDLOPHTSINGKAINQGNFASATMR-----GSD 596
Qy      587 LDINMGVVASDNTVPLDINVT-----FNSGTQFELNMIMFVPTNL 628
Db      597 LDYKTRTVGFTTPSPFLDQSTFTIGAMNFSGNEVYIDRIEFPVEV 645

RESULT 8
085796 PRELIMINARY; PRT; 719 AA.
AC 085796;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Insecticidal protein.
GN CRV101
OS Bacillus thuringiensis (subsp. kurstaki).
OC Plasmid large plasmid.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=29339;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SI01;
RA Zhong Q., Deng R., Long Q., Yuan M., Pang Y., Wang X.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF076953; AAC26910.1; -.
DR HSPF: P02965; ICY.
DR InterPro: IPR001178; Endotoxin.
DR InterPro: IPR005638; endotoxin_C.
DR InterPro: IPR005639; endotoxin_N.
DR Pfam: PF00555; endotoxin_1.
DR Pfam: PF03944; endotoxin_C; 1.
DR Pfam: PF03945; endotoxin_N; 1.
KW Plasmid.
SQ SEQUENCE 719 AA; 81230 MM; 42746D478359BBA7 CRC64;
Query Match 9.8%; Score 325.5; DB 2; length 719;

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Best Local Similarity 22.7%; Pred. No. 1,6e-13;
Matches 161; Conservative 103; Mismatches 272; Indels 173; Gaps 32;

Qy      21 HDPFSEHKK-----SIDTIRKEM-MEWRKTDH-----SLV--VAP----- 52
Db      9 HOSFSSNAVDKISTDLSLKNMETDIEIQNINMEDCLAKSEVENPEPVASITQIGIGIAG 68
Qy      53 -IYGTSSSLAKKQVSLGKRIISLMLGILPPSGTVMODILRETEFLNQRNTDTLLA 111
Db      69 KILGTLGVPPAGQVSLY-SFILGELM-----PKGK-NQMEIFMEHVEEIIINQKISTYARN 122
Qy      112 RVNALEGLQANIRENQOVDFINPTQNPVLSIT-SSVNTMOQLFNLPPFRVQGY 170
Db      123 KALTDKLGIDALAVYHDSLESWGNRRASVAKSYIALBELMFOKLSFAVSGEE 182
Qy      171 LLLPLPFOAANMLSPFRDVLVLADEWGISAAATLRTYQNTLKNYTESNYCINTYQTA 230
Db      183 VPLPPIYAOANLHLMLLDASIFGKEWGLSSSEISTFYNQOVERADYSDHCWKVYSTG 242
Qy      231 FRGL-NTRLHML--EFTYVFLNVEYVSIWLSFKYOSLIVSSGANL-----YASGSGP 282
Db      243 LNNLRGTNAESWVRVYQFRDMLTMDLVALPSPYDQMPITKTAQLTREYTDALGT 302
Qy      283 QQTQ-SFTSQDW-----PFL-----YSLPQVNSN-YVINGFSG 313
Db      303 VHPHSFTSTTWNANNAPEFSAIEAAVVRNPHLDLFLQVITYSLSRMSNTQYMMWMC3 362
Qy      314 ARLQTPPNIGLPGTTTHALLAARVNVSGVSGDIGAVFNQFSCSTPLPPLTPPV 373
Db      363 HKL--EFTTIGTLINIST-----QGSTNTSINPVLTPFT 394
Qy      374 RSWLDSGSDRGVNVTV-----NMQ--TESPESTLGLRCGAFTRAGNSYPPD 419
Db      395 SRDVRTESLAGNLPLTPQVNGVRVDPHKVFTHPIAS-----DNFYYPG 441
Qy      420 YFIRNISGVPLVVRNEDLRPLHNEIRNIESPGTGGRLAAYVSVHNRKNNTIYA-VHE 478
Db      442 Y-----AGIGTQLODSENELPPEATQPNYESYSHLSHG-LISASHKALVYSWTHR 494
Qy      479 NGTMHLAPEDYGTFTISPIHATQV-----NQRTTFISEKFG-NQGSRLREGSNTTA 531
Db      495 SA-----DRTN-TIEPNSITQIPLVKAFLSSGAAYVGRGFTGDIIR-RITVGT 543
Qy      532 RYTLRNGN-----GNSYNLRYVSLNSSTIRVTINGRYTASVNTTTNDGVNDGARF 586
Db      544 FGDIRVNIKPPAQRVIRVASTDLOPHTSINGKAINQGNFASATMR-----GSD 596
Qy      587 LDINMGVVASDNTVPLDINVT-----FNSGTQFELNMIMFVPTNL 628
Db      597 LDYKTRTVGFTTPSPFLDQSTFTIGAMNFSGNEVYIDRIEFPVEV 645

RESULT 9
08K761 PRELIMINARY; PRT; 719 AA.
AC 08K761;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Cry.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RA Porcar M., Martinez C., Caballero P.;
RT "Identification and characterization of a novel cry gene from Bacillus thuringiensis."
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF278797; AA073516.1; -.
DR InterPro: IPR001178; Endotoxin.
DR InterPro: IPR005638; endotoxin_C.
DR InterPro: IPR005639; endotoxin_N.

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DR Pfam: PF00555; endotoxin; 1.
DR Pfam: PF03944; endotoxin C; 1.
DR Pfam: PF03945; endotoxin N; 1.
SQ SEQUENCE 719 AA; 80984 MW; 84F1287246264473 CRC64;

Query Match 9.8%; Score 323.5; DB 2; Length 719;
Best Local Similarity 22.7%; Pred. No. 2.1e-13;
Matches 160; Conservative 111; Mismatches 269; Indels 165; Gaps 34;

21 HDPEPEHK-----SDITIRKEM-MEWKRTDH-----SLY--VAP-----52
9 HQSFSSMAKVDKISTDSKNETDIELOINHHDCIKTSEVENPEVPSASTIQTGISIAG 68
53 -IVGTUSFLKKGSLIGKRIILSELMLIPSGSTNMODLREFECPINQRLNTDTLA 111
69 KILGTIGVPPAGVASTLY-SFLLGEML-----PKGR-NQMEIFMEHVEELINQKSTAVRN 122
112 RVNALEGLQANIRENOQVDFNLTQNPVLSIT--SVNTMOQLFLARLPQRYVQYQ 170
123 KALTDLKGDLALAVYHESLESVGNKNTRRASVVKQYIAELMFVQKLSFVAVSGEE 182
171 LLLPLFAQANMHLSPTRDVVLADEMGISAATLRTYQNYIKYTTESNYCINTYQTA 230
183 VPLPLFYAQNANHLHLRLDASIRKEMGSSSEISTFYNNQVBRAGDYSDHCVMKYSTG 242
231 FRGL-NTRLHDL-EPRTYFNLVFEYVSIKQSL--VSSGANL--YAGS 280
243 INNLRTGNAESWVRVYQFRKMTLMVLDLALFP--SYDTLVYPIKTTSQLREYVTAI 300
281 GP-QQTOSFTSQDW-----PFL-----YSLFOVNSN-YVLNGF 311
301 GYVHNASFSASTTWNANAPSSTIESAVVRNHLDFLEQVITYSLSRMSNTQYMMW 360
312 SCARLTQTFPNIGLPGTTTHALLAARVYSGVSSGDIGAVNQNQFSCFPLPLTP 371
361 GGHRL--EFTTIGMNTST-----QGSTNININPVLTP 392
372 FVRSLDGSDDGQGVVTV-----NMQ--TESFESTLGLRCGAFTRGNSNYF 417
393 FTSRNVYRTESLAGLMLFLTPVNGVPRVDFHMKFVTHPIAS-----DNFY 439
418 PLYFRNISCYPLVYVNEEDLRPLHYNEINISSPGTGGARAVYVNRKNITVA-V 476
440 PGY-----AGTQLODSENELPPTTQCPYVSHSLSHG--LISAHVYALVYMT 492
477 HENGTMIHAPEDYTGFTISPIHATQV-----NNOTRTISEKFG--NOGDSIRFQOST 529
493 HNSA-----DRTN-TIEPNSITQIPVAFVLSGAAYVRGPGFTGDILR--RTMT 541
530 TARTYLRNGN-----SYNLYLRVSLGNSITRTINGRVYASVNTTTNDGVNDGA 584
542 GTFGDRIVNNPPAQRYRIRKYSTDIDFHSINGKAINQGFSAITNMR-GEIDLK 600
585 RFLDINMGVVAADNTVPLDIN--TENSQTQFLANINFPVPLN 628
601 TFRVGTTPFSFSDVOSTFTIGANFSGNEVYIDRIEVEV 645

RESULT 10
Q9F0P8 PRELIMINARY; PRT; 719 AA.
AC Q9F0P8;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, last annotation update)
DE CRY11.
GN CRY11.
OS Bacillus thuringiensis.
OG Plasmid pBIC19.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN (1)
RP SEQUENCE FROM N.A.

RC STRAIN-BRC007;
RA Song F., Zhang J., Huang D., Li G.;
RT "The cloning of a novel cryII gene from Bacillus thuringiensis
strain..."
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF211190; A043526.1; --
DR HSSP; P02965; IC1Y.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR Pfam; PF00555; endotoxin; 1.
DR Pfam; PF03944; endotoxin C; 1.
DR Pfam; PF03945; endotoxin N; 1.
KW Plasmid.
SQ SEQUENCE 719 AA; 81025 MW; 7E17481922C4356 CRC64;

Query Match 9.8%; Score 317.5; DB 2; Length 719;
Best Local Similarity 22.7%; Pred. No. 5.4e-13;
Matches 154; Conservative 113; Mismatches 273; Indels 139; Gaps 32;

19 VADPR--SFHRSIDTIRKEMWKRTHSLVYA-PIVGVVSFLKKGSLIGKRIILS 75
37 INHEDLMSHESID-----PVASSTIQTIGIGAKILGTIGVPPAGVASTLY-SFLLG 91
76 ELWGLIFSGSTNLMQDILRETEQFLNORLNTDTLARVALEGLQANIRENOQVDFN 135
92 ELW-----PKGSKQ--WEIFMEHVEELIDKISTYARNIALDLKGLDALVYHESLESWI 146
136 NPTQNPVLSIT--SVNTMOQLFLARLPQRYVQYQQLLLPLFAQANMHLSPTRDV 194
147 KKNMNAISVYKQYIAELFVQKLSFVAVSGEVPPLFYAQNANHLHLRLDASVF 206
195 ADEMGISAATLRTYQNYIKYTTESNYCINTYQTAIRGL-NTRLHDL-EPRTYME 250
207 GKEMGLNSQISTFENQOVERISDSDHCVMKYSTGANLRGNAESWVRVYQFRKMTL 266
251 NVEEYVSIKQSL--VSSGANL--YAGSGP-QQTOSFTSQDW-----293
267 MVLDLALFP--SYDTLVYPIKTTSQLREYVTAIQTVPNAPSASTTWNANAPSFS 324
294 -----PFL-----YSLFOVNSN-YVLNGFSGARLTQTFPNIGLPGTTTHAL 335
325 TESAIVANPHLDFLEQVITYSLSRMSNTQYMMWGHLL--EFTTIGVLTNTST----- 378
336 LAARVYSGVSSGDIGAVNQNQFSCFPLPLTPVRSMLDSDGQGVVTV----- 390
379 -----QGSTNININPVLTPFSRNVYRTESLAGLMLFLTPVNGVPRVDFHMKF 416
391 -----NMQTESFESTLGLRCGAFTRGNSNYFEDYFINNISGVDLVYVNEEDLR 443
417 GVPVDFHMKF-----ALPIASDNF-----YLAGY-----AGVGTQLODSENELP 460
444 NEINISPSGTGGARAVYVNRKNITVA-VHENGTMIHAPEDYTGFTISPIHATQ 502
461 TQCPYVSHSLSHG--LISAHVYALVYMTIRSA-----DRTN-TIEPNSITQ 509
503 V-----NNOTRTISEKFG--NOGDSIRFQOSTTARTYLRNGN-----SYNLY 550
510 IPLVAFNLSGAAYVRGPGFTGDILR--RTMTGTFGDRIVNNPPAQRYRIRKYST 567
551 LGNSTIRVINGRVYASVNTTTNDGVNDGAFELDINMGVVAADNTVPLDIN--T 609
568 TTDLQFHTSINGKAINQGFSAITNMR-GEIDLKTFRFGVGTTPFSFSDVOSTFTIG 626
610 FNSGTQFLANINFPVPLN 628
627 FSSGNEVYIDRIEVEV 645

RESULT 11
Q9S5V8 PRELIMINARY; PRT; 1180 AA.
AC Q9S5V8;
Q9S5V8;

DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
 DE Bt8441 crystal protein (Crystal protein Cry1A).
 GN Bt8441.
 OS Bacillus thuringiensis, and
 OS Bacillus thuringiensis (subsp. sotto).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_Taxid=1428, 29340;
 RN [1]
 RC SEQUENCE FROM N.A.
 RA Nagamatsu Y.;
 RU Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 RL [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES=B. thuringiensis; STRAIN=T84A1;
 RA Ogo M., Yamada S., Kobayashi Y., Shibata J., Nagamatsu Y.;
 RT "Nucleotide Sequence of the Lepidoptera-toxic Protein Gene of Bacillus thuringiensis subsp. dendrolimus T84A1.";
 RL J. Fac. Appl. Biol. Sci. Hiroshima Univ. 29:95-107 (1990).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC SPECIES=B. thuringiensis; STRAIN=T84A1;
 RA Nagamatsu Y., Itai Y., Hatanaka C., Funatsu G., Hayashi K.;
 RT "A Toxic Fragment from the Entomocidal Crystalline Protein of Bacillus thuringiensis.";
 RL Agric. Biol. Chem. 48:611-619 (1984).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC SPECIES=B. thuringiensis (subsp. sotto);
 RA Zhong W.F., Cai P.Z., Yan W.Z., Zhang X.X., Xiang Y.W.;
 RT "A cDNA gene cloned from Bacillus thuringiensis serovar sotto.";
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB026261; BAA77213.1;
 DR EMBL; AF510713; AA44305.1;
 DR HSSP; P02965.1C1Y;
 DR InterPro; IPR001178; Endotoxin.
 DR InterPro; IPR005638; endotoxin_C.
 DR InterPro; IPR005639; endotoxin_N.
 DR Pfam; PF00555; endotoxin_1.
 DR Pfam; PF03944; endotoxin_C.1.
 DR Pfam; PF03945; endotoxin_N.1.
 SQ SEQUENCE 1180 AA; 133489 MW; 1199546D1DC62D CRC64;
 Query Match 8.5%; Score 280.5; DB 2; Length 1180;
 Best Local Similarity 21.7%; Pred. No. 3.4e-10;
 Matches 152; Conservative 104; Mismatches 272; Indels 173; Gaps 29;
 QY 6 NNGRTTCDAVAVVAHDPFSEHKSIDTIRKEMEMKRT--DHSLYVAPVGVSSFLK 63
 DB 3 NNNINIECIPNCIS-----NPEVAVGGERIEGTYPIDIS-----SLTQFLLS 48
 QY 64 K-----VGLIKRILSLKGLIPSGSTNLMODILRETFQFNOIRLNDTLAVNMLEG 119
 DB 49 EAVPAGAVLD--LVDIWGIQGPS---QMDAVLQIQLINQRIEFARNAQISRLG 102
 QY 120 IQ-----ANIREFNOVDNPLNPTQNPVPLSTSSVNTMQQLFNRLPQPVQYQL 172
 DB 103 LSNLYQIYAESFREWE-----ADPTNPALEERKORPDMSALTINLPLFAVQYQVP 156
 QY 173 LILPFAOANMHLSTFEDVVLNADWEGISAATLFTYQNTLKNYTESNVCINTYQAFR 232
 DB 157 LLSVYVQANILHLSVLRDVSFGQWGFDAATINSRYNDLTGLTGNVDAVAVWYGL 216
 QY 233 ---GLATRLHML--EFTYVFLNVEEYVSIKFKYQSLIVSSGANLYASGSGQOQ 286
 DB 217 RVWGPDNR--DWRYNQFRELTLVLDIALPS-----NDSRRPIKTIV 260
 QY 287 SFTSQDWPFYLSLFQVNSNYVNGPSG-----RLTQTF--PIIGLPGTTTALIAA 338
 DB 261 SGLTR-----ELYNPVLNFDSFGMAQRLEQNIQRIOPHLMIDILNRIITYTDVHR 311

QY 339 RVNYSG--VSSGIDGAVFNONPSCSTF-----LPLLTLP----- 371
 DB 312 GPVWSSHQITLSPVG-----FGGEFAPPLFGNAGNAAPVYLVTGIGFTLSSPL 365
 QY 372 FVRSMIDSGSDRGVNTVNMQTESFSTLGRCAFPAGNAGNYPDPVFINISGVPLV 431
 DB 366 YRRIILSGPNNQELFVLDGERSFASLTNLPSTIRKQKT-----VSLDVLTPQ 417
 QY 432 VRNEDLRRLAH--NEIKNIPSPSGTIPGGLRANVSVHNRK--NNIYAVH----- 478
 DB 418 DNSVPPAGFSRLSHVTMLSQAGAVYTLRAPFSSQHRSAEFNNIIPSSQITQIPLT 477
 QY 479 -----NGTMILHAPEDYGEFTISPIHATQVNNQRTFISKFGQSGSLRFEQNTARY 533
 DB 478 STYLSGTSVAVKGP-----GFT-----GGDILR--RTSPQOIS 508
 QY 534 TLGN-----GNSVNLKRVSSIGNSTIRVYTNNGRYTASVNTTNDGVNDGARFLD 588
 DB 509 TLKVNITAPLSQRTKRVIRYASTTNLQFHTSIDRPINQGNFSAWSS--GSLQSGSFT 567
 QY 589 INNGNVASDNTNPVLDINV--TENSQTFELMNIIMFVPTNL 628
 DB 568 VGFTTFPNSGSSVFTLSAHVFNSGNEVYIDRIEFVPAEV 608
 RESULT 12
 ID 098603 PRELIMINARY; PRT; 645 AA.
 AC 098603
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
 DE Delta-endotoxin (Fragment).
 OS Bacillus thuringiensis
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_Taxid=1428;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=serovar japonensis type;
 RA MEDLINE=99025985; PubMed=9806979;
 RA Maeno N., Ohba M.;
 RT "Assignment of delta-endotoxin genes of the four lepidoptera-specific Bacillus thuringiensis strains that produce spherical parasporal inclusions.";
 RL Curr. Microbiol. 37:408-411 (1998).
 DR EMBL; AF042733; AAB97923.1;
 DR HSSP; P07130; IDLC.
 DR InterPro; IPR001178; Endotoxin.
 DR InterPro; IPR005638; endotoxin_C.
 DR InterPro; IPR005639; endotoxin_N.
 DR Pfam; PF00555; endotoxin_1.
 DR Pfam; PF03944; endotoxin_C.1.
 DR Pfam; PF03945; endotoxin_N.1.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 645 AA; 72967 MW; 143B51312B890CE3 CRC64;
 Query Match 8.4%; Score 279.5; DB 2; Length 645;
 Best Local Similarity 22.1%; Pred. No. 1.7e-10;
 Matches 149; Conservative 94; Mismatches 276; Indels 155; Gaps 28;
 QY 13 CDAYNVADHPSPFSEHKSIDTIRKEMEMKRTDHSLYVAPVGVSSFLK 69
 DB 4 CPADVDVKTPLTDDNAGLQNM--NYKELTYGGDYDPLINPNISVSGKDVIGQVGINI 61
 QY 70 GKRLIS-----ELMGLIPSGSTNLMODILRETFQFNOIRLNDTLAVNMLEG 114
 DB 62 VGRILSFSGFPSSQWTVYTYVLNLSWPDENSWMAPFEREHEIIDOKISEAVKRAL 121
 QY 115 AEELEGQANIREFNOVDNPLNPTQNPVPLSTSSVNTMQQLFNRLPQPVQYQL 170
 DB 122 DDLNLGQVYNNLYBALDNLNRPNGARASLVISQRFNIIISLFTQFMPSFGSGGQNTA 181

QY 171 LLLPLPAAAMHLSFIRDVVNLADENGISAAATRTYQNYLKNYTTESVNCINTYQTA 230
 DB 182 TLLPVAOAAHMLLLKADYKARKMLNQTQIDFHSRQOSLTQYTNHCVTAINGD 241
 QY 231 FRGL-WTRLDHMLEFRY--MFLNFEYVLSLFFKQSLVSSGAMVSSGSGPQOQ 286
 DB 242 LAELRGTAESWFKNQYRREMTLAMDV--ALFPYVNL--ROYPDGNPQUR 292
 QY 287 SF-----TSQ--DW-----PFLV--SLFQVNSN 305
 DB 293 EYTDPLADPLEOFTTQCSWYINPAPRNHNFVLENSLRPHELPERLSMLQILV 352
 QY 306 YVING--FSGARLTOTFPNIGLPGTTTHALLARVYVSSGSDIGAVNOMFGSCT 363
 DB 353 YOTGSAVRGSRVRYHYHSSIT--QEKSYGLSDPVGAMNQNNDIYQIISQ--VSN 407
 QY 364 FLPLPLTFP--VSMDSGSDRG--GVNTVNMQTSFESTLGLRCAFTARG 412
 DB 408 FASPVSSTSVMDTPNVLSSGVGIGYTOGSIYAVCLQQRNSTELPSLMEGDIIRN 467
 QY 413 NS--NFPDY-FIRNIGVPLV-----RNEDLRPLHNEIRNI-----ES 451
 DB 468 YSHRLSHITQRFQATGSSPSSTVSNLPTCWTHTRDVLDLNTITANOITQLPVKAYEL 527
 QY 452 PSG-----TPGLRAYVSVNRKNNIYAVHENGTMHILAPEDYGF 493
 DB 528 SSGATVYKPGFTGQDVIRRTGTGFGAIVSVTGLTORVRI--FRYATIDPFF 583
 QY 494 TISPLHATQVNN--QRTTISKFGNQGDSLRFEGSNTTAYTRGNSYMLYRVSLS 551
 DB 584 VTR--GGTTNNFRFRITM-----NRGQSRKE-SYRIVEFTTPNFQSDIIRTSIQ 634
 QY 552 GNSITRVINGRYV 565
 DB 635 GLSG-----NGEVY 643

RESULT 13
 ID Q93NMS PRELIMINARY; PRT; 1228 AA.
 AC Q93NMS;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
 DE CRY1BA.
 GN CRY1BA.
 OS Bacillus thuringiensis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1428;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhang J., Song F., Huang D.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF368257; AK63251.1; -
 DR InterPro; IPR001178; Endotoxin.
 DR InterPro; IPR005639; endotoxin_C.
 DR InterPro; IPR005639; endotoxin_N.
 DR Pfam; PF00555; endotoxin_1.
 DR Pfam; PF03944; endotoxin_C1.
 DR Pfam; PF03945; endotoxin_N_1.
 SQ SEQUENCE 1228 AA; 13966 MW; E86D9842341F439 CRC64;

Query Match 8.4%; Score 278.5; DB 2; Length 1228;
 Best Local Similarity 22.1%; Pred. No. 4.8e-10;
 Matches 152; Conservative 100; Mismatches 228; Indels 209; Gaps 33;
 DB 68 PFAQOLASFYSFLV-----ELM--PRG--RDWEI-FLEHVEQLINQITENARN 113
 QY 52 PIVGVSSFLKKVSLIGKRIISLWGLIFPSSGTNIMODILRETEQINQINQITENARN 111
 DB 112 RVNALELGQANIREFNOQVNFNPONVPLSTSSVNTMOOL-FINRLPQRFVQGYQ 170
 QY 114 TALARKLGSDSRFAYQSLDWMLENRDARFRSVLYTYVIALELDFLNAMPLFAIRNOE 173

QY 171 LLLPLPAAAMHLSFIRDVVNLADENGISAAATRTYQNYLKNYTTESVNCINTYQTA 229
 DB 174 VPLLVAOAAHMLLLKADYKARKMLNQTQIDFHSRQOSLTQYTNHCVTAINGD 233
 QY 230 --AFRGLN--TRLDHMLEFRY--MFLNFEYVLSLFFKQSLVSSGAMVSSGSGPQOQ 279
 DB 234 LMSLGRTAASWVRVY--QFRRLDILGLDVALPSPYDRTYPTINSAQLTREVYIDA 290
 QY 280 SSGQGTGSGSDM-----PFL-----YSLFQVNSVY--LNGF 311
 DB 291 IGATGV-NMASMWNVNNAPSPSALEAARSPHLDPLEQLIFSAASRWSNTRMTY 349
 QY 312 SGARLTOTFPNIGLPGTTTHALLARVY-----YSGVSSGSDIGAVF 355
 DB 350 RG-RTIGSRPIGGGL--NTSTGATNTSINLVTLRASADVRYTESAGVLLWG----- 400
 QY 356 NQFSGSTFLPLPLTFPVASWIDSGSDRGVNTV--TNWQTSFESTLGLRCAFTAR 411
 DB 401 -----ITLPEI-----HGVPTVRNFTNPQN-----ISDR 425
 QY 412 GNSNFPDYFRNIGSVPLVWNEDLRRLHNEIRNISPGTQGLRAYVSVNRKN 471
 DB 426 GTANYSQPY-----ESPGQLQKDSFELPPTERRNYSYSHR--LSHGIIILQSRV 477
 QY 472 -NITYA-VHENGTMHILAPEDYGFITISPIHATQVNNQRTFISEKFGNQGDSLRFEGSNT 529
 DB 478 VPVYSWTRSA-----DRTN-TIGPNRITQI--PMVKASLPGTTV----- 516
 QY 530 TARTLRKNG-NSNLYLARSLSGNSITRVING-----RVYASVWNTTNNNG 578
 DB 517 --VRGGFTGQDILKRTNIGGPGPIRVYVNGPLQRIRIGFYASTVDFDFVSRGG 571
 QY 579 VINDGARFL-----DINMGNV-----ASDNTNPLD-- 605
 DB 572 TTVNNFRFLRTNNSGDELKYGNEFRAPFTPTPTQIQQIIRTSIQGLSGNGEYIIXLE 631
 QY 606 -INVTNSGTQPEL-----MNIMFVPTN 627
 DB 632 IIPVATTFEAYIDLERQAEVNAALFTNTN 660

RESULT 14
 ID Q45740 PRELIMINARY; PRT; 381 AA.
 AC Q45740;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
 DE Insecticidal crystal protein (CryII) (Fragment).
 OS Bacillus thuringiensis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1428;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=EG6346;
 RX MEDLINE=91286178; PubMed=2061280;
 RA Chambers J.A., Jelen A., Gilbert M.P., Jany C.S., Johnson T.B.,
 RA Gawron-Burke C.;
 RT "Isolation and characterization of a novel insecticidal crystal
 protein gene from Bacillus thuringiensis subsp. aizawai.";
 RL J. Bacteriol. 173:3966-3976(1991).
 DR EMBL; M63897; AAA2349.1; -
 DR HSP; P07130; IDC.
 DR InterPro; IPR001178; Endotoxin.
 DR InterPro; IPR005639; endotoxin_N.
 DR Pfam; PF00555; endotoxin_1.
 DR Pfam; PF03945; endotoxin_N_1.
 FT NON TER 381
 SQ SEQUENCE 381 AA; 42967 MW; DDAEF0D0504CE36C CRC64;

Query Match 8.4%; Score 277.5; DB 2; Length 381;
 Best Local Similarity 26.3%; Pred. No. 1.1e-10;

Matches 100; Conservative 66; Mismatches 135; Indels 79; Gaps 19;

QY 21 HDPSEFEHK-----SLDTIRKEM-MEMKRTDH-----SLY-VAP-----52
 Db 9 HOSFSSNAKYDKISTDSTLKNETDIEIQNHHECKLISEYENVEPVSASTIOTIGISAG 68
 QY 53 -YGVVSPFLKKVGLSLQKRLISELWGLIFPGSGTNLMODILRETEQFLNRLTDTLA 111
 Db 69 KLTGTLVPPAGQVAVSLY-SFLLEBLM-----PFGK-NQWEI-FMEHVEIILNOKISTYARN 122
 QY 112 RVNALEGLQANIRENOQVNFPLNTPONFVPLST-SVNTWQOQLFNLRFQFVQYQ 170
 Db 123 KALYDLKGLDALAYVHESLESSESWGNKNTBRASVYKQYALALEMVFQKLSFVSGEE 182
 QY 171 LLLPLFOAANHLSPTRDVLNADDEWGISAAITLFTYQNTLYKNYTESYNYCINTYQTA 230
 Db 183 VPLPIYQANHLHLILRLDASIFGKESWGLSSSEISTEYNQVERAGDYSDHCVMYSTG 242
 QY 231 FRGL-NTRLHDL-----EFRTYMLNVEYVSIWLFKYQSL--VSSGANL---VASGS 280
 Db 243 LNNLRGTNAESWVRVNOFRKDMTLMVLVALFP--SYDLVYPIKTSQLRREYTDAL 300
 QY 281 GP--QOTQSFSTQDW-----PEL-----YSLFQVNSN-YVANGF 311
 Db 301 GYVNPVASFSTYTNVNNNAPSFRTIESAVVRNPHLDLEQVTTYSLSRMSNTQYNNMW 360
 QY 312 SGARLQTPNPNGILPGTTT 331
 Db 361 GGRHL--EFFRTIGMLNTST 378

RESULT 15

Q45720 PRELIMINARY; PRT; 620 AA.
 AC Q45720
 DT 01-NOV-1996 (TEMBLrel. 01, Created)
 BT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
 DT 01-OCT-2002 (TEMBLrel. 22, Last annotation update)
 DE CRYIA(a) (Fragment).
 GN CRYIA(a).
 OS Bacillus thuringiensis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1428;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-NRD-12;
 RX MEDLINE=95386467; PubMed=7657602;
 RA Maeson L., Lu Y.J., Mazza A., Brousseau R.,
 RT "The CRYIA(c) receptor purified from Manduca sexta displays multiple
 specificities.";
 RL J. Biol. Chem. 270:20309-20315(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-NRD-12;
 RX MEDLINE=95231292; PubMed=7715447;
 RA Maeson L., Mazza A., Gringorten L., Baines D., Anelinas V.,
 RT "Specificity domain localization of Bacillus thuringiensis
 insecticidal toxins is highly dependent on the bioassay system.";
 RL Mol. Microbiol. 14:851-860(1994).
 DR EMBL; U43605; AAA86265.1; -
 DR HSSP; P02965; ICIY
 DR InterPro; IPR001176; Endotoxin.
 DR InterPro; IPR005638; endotoxin_C.
 DR InterPro; IPR005639; endotoxin_N.
 DR Pfam; PF003944; endotoxin_C; 1.
 DR Pfam; PF003945; endotoxin_N; 1.
 FT NON TER 1
 SQ SEQUENCE 620 AA; 69428 MW; 4571A09E5656EDE CRC64;

Query Match

8.3%; Score 276.5; DB 2; Length 620;

Best Local Similarity 21.5%; Pred. No. 2.5e-10;
 Matches 151; Conservative 105; Mismatches 272; Indels 173; Gaps 29;

QY 6 NNGRTTICDANNVVAHDPSEFEHKSLDTIRKEMEMKRT--DHSLYVAIVGTYSFLK 63
 Db 3 NNPNINECIPIVNCIS-----NPEVVGSRRIETGTIPIDISL-----SLQFLLS 48
 QY 64 K-----VGSILGRILISELWGLIFPGSGTNLMODILRETEQFLNRLTDTLARVNALEGL 119
 Db 49 EYVPGAFVPLG--LVLDIWIQIFGRS---QMDAVLQVIEQLINQRIIEEPARNQVLSLEG 102
 QY 120 LQ-----ANIRENOQVNFPLNTPONFVPLSTSSVNTWQOQLFNLRFQFVQYQ 172
 Db 103 LSNLYQIYAESPREWE-----ADPTNPLABEKRIQIPNDMSALTYAIPLAIVQYV 156
 QY 173 LLLPLFOAANHLSPTRDVLNADDEWGISAAITLFTYQNTLYKNYTESYNYCINTYQTA 232
 Db 157 LLSVYQANHLHLILRLDASIFGKESWGLSSSEISTEYNQVERAGDYSDHCVMYSTG 242
 QY 233 --GLNTRLHDL-----EFRTYMLNVEYVSIWLFKYQSL--VSSGANL--VASGS 280
 Db 217 RVNGPDSR--DMVRYNQFRRELTLVLDIVALFS-----NYDSRRYPIRTV 260
 QY 287 SFTSQDWPFVLSLQVNSVNLNGSGA-----RLTQTF--PNIGLPGTTTHALLAA 338
 Db 261 SOLTR-----EITNPEVLNFDSSFRGMQRLEQNIROPHIMDLINSITTYDVHR 311
 QY 339 RVNYSGG--VSSGDIGAVRNQFSCSTP-----LPLPLTP-----371
 Db 312 GFNYVSGHQLTASPVG-----FSGPEFAPPLFGNAGNAPVLVSLGIGIRTLSSPL 365
 QY 372 FVRSWLDGSDRGGVNTVNTMOTSEFESTGLRCGAFTRGNSNTPDYTRINISGPLY 431
 Db 366 YRRIILSGPRNQDELVLDTGEFASLITNLPSSTIRQGT-----VDSLIVIPQ 417
 QY 432 VNEEDLRPLHY--NIRNISEPSCGTGGLRAYMVSVNRK--NNIYAVE-----478
 Db 418 DNSVPPRAGFSLHSHVTMLSQAGAAVYTLRAPTFESQWRSSEFNIIIPSSQITQPLTK 477
 QY 479 -----NGTMHLAPEDYTGFTISPIHATVQNNQTRFISEKFGQSGSLARFESNTARY 533
 Db 478 STNLSSGTSVVKGPD-----GFT-----GSDILK--RTSQQIS 508
 QY 534 TLRGN-----GNSYNYLAVSSLSNGSTIRVTNGRVYASVNTTTNDGVNDGARFLD 588
 Db 509 TLKVVITAPLSQRYRVRIRYASTTNLQPHTSIDGRPIHQGFSAIWS--GSLQSGSFRT 567
 QY 589 INMGAVVASDNTVPLDINV--TNSGTQFELMNIHFVPTNL 628
 Db 568 VGFTTPPNFNSGSSVPTLSAHVFNSGMEVYIDRIEVPAAV 608

Search completed: August 14, 2003, 18:12:13
 Job time : 50 secs

